

AUTHOR INDEX

VOLUME 11

- Aaronson, Stuart A., 134, 3780
 Abastado, Jean-Pierre, 486
 Abate, Cory, 3624
 Abdollahi, Abbas, 4371
 Aberdam, Daniel, 554
 Abraham, Robert T., 4431
 Abravaya, Klara, 586
 Achacoso, Philip, 440
 Adachi, Yasuhisa, 2567
 Adam, Gerhard, 699
 Adam, Rodney D., 3326
 Adelman, John P., 2547
 Adler, Brian K., 5878
 Aebersold, Ruedi, 2517
 Afar, Daniel E. H., 568
 Akeson, Richard, 1654
 Akiyama, Tetsu, 833, 6279
 Aksoy, Serap, 6139
 Alamo, Isaac, Jr., 1009
 Alani, Rhoda, 6286
 Albitar, Maher, 3786
 Alemà, Stefano, 3331
 Alessandrini, Alessandro, 2096
 Alexander, Stephen, 3171
 Alexandropoulos, Konstantina, 102
 Alitalo, Kari, 4015
 Allis, C. David, 166, 1729
 Almouzni, Geneviève, 655
 Aloni, Yosef, 1195, 3515
 Alonso-Caplen, Firelli V., 1092
 Al-Shawi, Raya, 4207
 Alt, Frederick, 5551
 Alt, Frederick W., 440, 1770
 Amalric, François, 573
 Amin, Anthony, 4497
 Amin, Jahanshah, 3660, 5937
 Anderson, Dirk, 3020
 Anderson, Dirk M., 3043
 Anderson, G. Mark, 1935
 Anderson, Matthew P., 3886
 Andersson, Agneta, 2125
 Andreetta, Francesca, 1631
 Andrews, David W., 2656
 Angel, Peter, 6286
 Annarella, Mary B., 2189
 Aoyama, Akira, 803
 Aplan, Peter D., 5462
 App, Harald, 913
 Appel, Frank, 5137
 Arai, Ken-ichi, 5894
 Arai, Naoko, 5894
 Araki, Shin, 1438
 Archer, Trevor K., 688
 Armstrong, Robert C., 4739
 Arndt, Kim T., 2133, 3642
 Arnheim, Norman, 1813
 Arrick, Bradley A., 4306
 Aspenström, Pontus, 213
 Atchison, Michael L., 1040
 Atkinson, Tom, 329
 Attardi, Giuseppe, 2236
 Aufderheide, Karl, 1133
 Auger, Elizabeth A., 6034
 Augustine, Andrew, 3454
 Augustine, James A., 4431
 Avruch, Joseph, 5541
 Axelrod, Amy, 1080
 Axelrod, Jeffrey D., 564
 Ayyub, Helena, 4679
 Azizkhan, Jane Clifford, 4943
 Bacher, Nina, 126
 Baer, Richard, 3037
 Baeuerle, Patrick A., 1017
 Bagchi, Milan K., 4998
 Balasubramanyam, Ashok, 5541
 Baldwin, Albert S., Jr., 4943
 Ball, Roland K., 3745
 Ballantyne, Scott M., 1713
 Baltimore, David, 1107, 1156, 1431, 5603
 Banerjee, Paria, 5541
 Banerji, Sunandita S., 4074
 Banker, Deborah E., 5079
 Barber, Glen N., 5497
 Barden, Nicholas, 1647
 Barker, Douglas D., 5154
 Barker, George F., 2760
 Barklis, Eric, 1214
 Barlowe, Charles, 5727
 Barnett, Stanley F., 864
 Baron, Margaret H., 1239
 Barrett, John, 954
 Barrett, Susanna F., 1009
 Bartel, David P., 3390
 Bartholomew, Blaine, 5181
 Bartholomew, Christopher, 1820
 Baserga, Renato, 731
 Basilico, Claudio, 1138, 6059
 Bates, Brian, 1840
 Batra, Janendra K., 2200
 Baumann, Heinz, 3001
 Bautista, Carmelita, 5792
 Bear, Susan E., 2864
 Beard, Charles B., 6139
 Beato, Miguel, 3247
 Becherer, Kathleen, 5801
 Becker, Jeffrey M., 1030, 3603
 Beecham, Edward J., 3095
 Beeler, David L., 6116
 Beemon, Karen, 2760
 Beg, Amer A., 4943
 Beidler, David R., 987
 Belin, Dominique, 2826
 Bell, John C., 568
 Bellacosa, Alfonso, 2864
 Bellard, Maria, 523
 Bellot, F., 5068
 Benbow, Robert M., 299
 Benchimol, Samuel, 1
 Bender, Alan, 1295
 Benezra, Robert, 6185
 Bengal, Eyal, 1195, 3515
 Bensch, K. G., 632
 Bentley, Rex C., 1829
 Berard, Diana S., 2529
 Berberof, Magali, 1473
 Berent, Eva, 126
 Berg, Paul, 445
 Berger, Edward M., 1846
 Bergsma, Derk J., 1718
 Berk, Arnold J., 63
 Berns, Anton, 1176
 Bernstein, Alan, 3043
 Berrodin, Thomas J., 5005
 Bertrand, Karen I., 5878
 Best, Lewis, 1069
 Beyer, Ann L., 3823
 Bigler, Jeannette, 5079
 Binder, Michael, 4104
 Bindereif, Albrecht, 2026, 5516
 Binétruy, Bernard, 6286
 Birrer, Michael J., 6286
 Bishop, J. Michael, 226, 4760, 5446
 Bishop, John O., 4207
 Bisson, Linda F., 3804
 Blair, Donald G., 604
 Blanchard, Jean-Marie, 2826, 2832
 Blanchard, Rachel A., 3132, 6158
 Blatt, Cila, 554
 Blenis, John, 1861, 1868
 Blumenthal, Thomas, 1921, 4651
 Boayke, Ken A., 5639
 Boeke, Jef D., 2736
 Bogenhagen, Daniel F., 4441
 Bohjanen, Paul R., 3288
 Böhm, Ruth, 2416
 Bohr, Vilhelm A., 3095
 Bokoch, G. M., 1523
 Bolen, Joseph B., 2391
 Bollag, Roni J., 4839
 Boncinelli, Eduardo, 3573
 Bonilla, Eduardo, 1631
 Bonneaud, Nathalie, 3075
 Bonner, José, 4555
 Boonchird, Chuenchit, 2852
 Boothby, Mark, 5551
 Bornstein, Paul, 2066
 Bos, Johannes L., 5963
 Bostian, Keith A., 4616
 Bottaro, Donald P., 3191
 Boulet, Isabelle, 3399, 4363
 Bouton, Amy H., 945
 Bouvet, P., 3115
 Bowen, Josephine K., 166
 Bowman, Tammy L., 2929
 Boyer, Bert B., 4147
 Boyer, Jayne C., 3711
 Boy-Marcotte, Emmanuelle, 202
 Bradley, Allan, 4509, 5586
 Bradshaw-Rouse, Judith, 4591
 Brambilla, Paolo, 6177
 Brand, Korbinian, 4732
 Brand, Stephen J., 2686
 Brandriss, Marjorie C., 564, 2609
 Brannan, Cami'ynn I., 3020
 Brasier, Allan R., 2887
 Braus, Gerhard H., 3060
 Bravo, Rodrigo, 381, 2451, 4466, 5470
 Brecht, Christian, 1171
 Breindl, Michael, 47, 5154
 Breitman, Martin L., 1531
 Brennan, Thomas J., 3633
 Brenner, Alfred A., 3369
 Brenner, David A., 4065
 Bresolin, Nereo, 2236
 Brewer, Gary, 2460
 Bricmont, Patricia A., 1161
 Brissette, Janice L., 5364
 Brizuela, Leonardo, 4616
 Broach, James R., 2641, 4045, 5346
 Brott, Barbara K., 5059
 Brown, Alistair J. P., 5330
 Brown, Julie A., 5301
 Brown, L. E., 2328
 Brown, Powell, 6286
 Brown, Steven D., 2467
 Brugge, Joan S., 4165, 4371, 4739
 Bruns, Gail, 3296
 Brunton, Laurie L., 3374
 Buckler, Alan J., 1707
 Budding, Mark, 3940
 Buettner, Reinhard, 3573
 Bugler, Beatrix, 573
 Bullock, Peter A., 2350
 Bumcrot, David A., 1048
 Bun-Ya, Masanori, 3229
 Burch, John B. E., 2704, 4863
 Burch, Robert, 5919
 Burd, Christopher G., 3419
 Burger, Gertraud, 795, 5746
 Burgess, Antony W., 4005
 Burke, Daniel J., 3691, 5592
 Burke, Joanne, 4207
 Buschman, Ellen, 595
 Buss, J. E., 1523
 Bussey, Howard, 175
 Bustin, Michael, 4483
 Butler, Geraldine, 476, 1232
 Butow, Ronald A., 38
 Buxton, David, 4207
 Byström, Anders S., 213
 Cafferkey, Robert, 1718
 Cairns, Bradley R., 240
 Calabretta, Bruno, 731, 6166
 Calame, Kathryn, 1765, 5197
 Calderwood, Stuart K., 3365
 Caldwell, Guy A., 3603
 Calos, Michele P., 1464, 2263
 Campbell, Frank E., Jr., 3978
 Canalis, Ernesto, 250, 4490
 Cantley, Lewis C., 1107
 Capobianco, Anthony J., 5867
 Carbon, John, 2206
 Cardelli, James A., 3339
 Cardillo, Thomas S., 5487
 Carey, John, 906
 Carey, Kendall, 4846
 Carlberg, Monika, 4876
 Carlstedt-Duke, Jan, 3379
 Carmichael, Gordon G., 5291
 Carroll, Dana, 3268, 3278
 Carroll, Robert B., 1598
 Carroll, Susan M., 4779
 Carter, Mary Corrigan, 2116
 Cartwright, Charles P., 2620
 Caruthers, Marvin H., 3475
 Casadevall, Carmen, 6166
 Casey, P. J., 1523
 Castillo, Gonzalo R., 3407
 Cavener, Douglas R., 2149
 Cawthon, Richard, 906
 Centrella, Michael, 250, 4490
 Cerruti, Martine, 1171
 Chacko, Sarah A., 4473
 Chain, Aileen C., 1538

- Chakraborty, Tushar, 3633, 6103
 Chalepakakis, Georges, 3247
 Chamberlain, John W., 3564
 Chan, Hedy, 47
 Chan, Jeannie, 5885
 Chandley, Ann, 4207
 Chang, Christine, 4509
 Chao, Chuck C.-K., 2075
 Chaudhary, Vijay K., 2200
 Chebli, Karim, 1258
 Chen, Helen, 4627
 Chen, Jiandong, 5968
 Chen, Lian-Sheng, 5222
 Chen, Qi, 3037
 Chen, Rey-Huei, 1861, 1868
 Chen, Ruey-Hwa, 1927
 Chen, Suzie, 3472
 Chen, Zhi, 6248
 Cheng, Jjin-Tsuey, 3037
 Cheng, Seng H., 3886
 Cheng, Yih-Shyun E., 4717
 Chevallier, M. R., 1114
 Chi, Tianhuai, 1754
 Chiang, Anne, 5710
 Chien, Kenneth R., 2273
 Chodchoy, Nunta, 497
 Choi, John K., 4473
 Choi, Ted, 3070
 Chomyn, Anne, 2236
 Chong, Karen, 5497
 Chow, King-Lau, 2439, 5090
 Chrebet, Gary, 4616
 Chu, Gilbert, 3348
 Chung, Hui-min, 2467
 Chung, Jongkyeong, 1861, 1868
 Church, Deanna, 3691
 Church, William R., 3537
 Cigan, A. Mark, 3203, 3217
 Citri, Yoav, 1017
 Clark, Alan B., 2576, 2583
 Clark, Chris D., 5710
 Clark, John T., 963
 Clark, Lauretta, 1590
 Clark, R., 1523
 Clarke, Louise, 2206
 Clarke, Margaret, 3339
 Clark-Walker, G. Desmond, 1662
 Clayton, David F., 1770
 Cleary, Michael L., 6149
 Cleveland, J. L., 1912
 Cline, Thomas W., 3584
 Cobb, Bradley S., 5832
 Coen, Donald M., 4786
 Coffey, Paul J., 5541
 Coffin, John M., 1419
 Cogswell, John P., 2406
 Cogswell, Patricia C., 5016
 Cohen, Gerald, 510
 Cohen, J. John, 4177
 Cohen-Kupiec, Rachel, 5275
 Collard, Michael W., 1448
 Collart, Frank R., 5417
 Collart, Martine A., 2826
 Collins, Kathleen L., 2108
 Collum, Robert G., 1770
 Colmenares, Clemencia, 1167
 Comoglio, Paolo, 5954
 Comoglio, Paolo M., 1793, 6084
 Conklin, Patricia L., 4274
 Conrad, Richard, 1921, 4651
 Conzelmann, Andreas, 27
 Coodly, Lavanya R., 4943
 Cook, Alistair C., 12
 Cook, John S., 2425
 Cook, Paul W., 2547
 Cook, Richard G., 166
 Cooper, Geoffrey M., 5190
 Cooper, Jonathan A., 2517
 Cooper, Terrance G., 1161, 6205
 Copeland, Neal G., 2665, 3020, 5603
 Cordingley, Michael G., 688, 2529
 Cordle, Susan R., 1734, 2881
 Coren, Jonathan S., 2282
 Coruzzi, Gloria, 4966
 Coschigano, Peter W., 822, 4455
 Costantini, Frank, 4244
 Couturier, Anne, 3395
 Cowman, Alan F., 5244
 Craig, Nessly, 458
 Crepaldi, Tiziana, 5954
 Croop, James M., 3940
 Crosby, Seth D., 3835
 Cross, Mike, 2026, 5516
 Cruzalegui, Francisco, 3960
 Cserjesi, Peter, 4854
 Culbertson, Michael R., 2629
 Culver, Melanie, 906
 Cunliff, Nina F. A., 3504
 Cunningham, Thomas S., 6205
 Curran, Tom, 3624
 Cuthill, Scott, 401, 4314
 Daar, Ira, 604
 Daar, Ira O., 5985
 Daley, George Q., 1107
 Damak, Faten, 202
 D'Andrea, Alan, 4895
 D'Andrea, Alan D., 1980
 Dang, Chi V., 954
 Danielpour, David, 5222
 Danner, David B., 1372
 D'Arcangelo, Gabriella, 4739
 Darlington, Gretchen J., 4423
 Darnell, James E., 182
 Darnell, James E., Jr., 5147, 6050
 Darrow, Andrew L., 3139
 Das, Chhaya, 5197, 5206
 Das, Gokul C., 1488
 Dascher, Christiane, 872, 2980
 Daugherty, Jon R., 1161
 Davis, Dorene L., 2704, 4863
 Davis, Ian J., 3239
 Davis, Lenora J., 3997
 Davis, Leslie R., 5346
 Davis, Roger A., 2049
 Davis, Terri, 3020
 Dawid, Igor B., 2481
 Dawson, Dean, 6328
 Day, Regina, 4830
 Dean, Ann, 2558
 Dean, Jurrien, 6197
 Deanda, Kristine, 4333
 de Belle, Ian, 2752
 De Benedetti, Arrigo, 5435
 Debinski, Waldemar, 1751
 deBruynKops, Anne, 4786
 DeCaprio, James A., 972
 Decker, Stuart, 5059
 Decker, Thomas, 182, 5147
 DeClue, Jeffrey E., 2819, 3132
 de Crombrughe, Benoit, 2291
 Dedon, Peter C., 1729
 Defeo-Jones, Deborah, 2307, 5792
 Degenstein, Linda, 5275
 de Groot, Rolf, 192
 deLannoy, Peter, 3425
 Dell'Orco, Robert, 1372
 DeMarco, Michael, 4371
 de Martin, Rainer, 5338
 Demediuk, Barbara, 2686
 Demple, Bruce, 4537
 d'Enfert, Christophe, 5727
 Denny, Christopher T., 1854
 Densmore, Lezlie, 154
 Dent, C. L., 3925
 DePaoli-Roach, Anna A., 5767
 DePinho, Ronald A., 6007
 Der, C. J., 1523
 Derman, Eva, 4244
 Derynck, Rik, 4306
 Desiderio, Stephen V., 2096, 6185
 Detloff, Peter, 737
 Devary, Yoram, 2804
 Devauchelle, Gérard, 1171
 Dever, Thomas E., 5992
 Devlin, Cecilia, 3642
 DeZazzo, James D., 1624, 5977
 Dhar, Veena, 6268
 Dickson, Clive, 5929
 Dickson, Robert C., 1777
 Dieckmann, Carol L., 813
 Di Fiore, Pier Paolo, 2040, 3191
 Digard, Paul, 4786
 Dijkwel, P. A., 3850
 Dildrop, Renate, 440
 DiMauro, Salvatore, 1631
 Di Nocera, Pier Paolo, 5171
 Dionne, C. A., 5068
 DiPersio, C. Michael, 773, 4405
 Dobens, Leonard, 1846
 Dobrowolski, Steven, 2785
 Dobrzanski, Pawel, 5470
 Doctor, John S., 2319
 Doi, Takefumi, 6116
 Domen, Jos, 1176
 Domenjoud, Lionel, 4581
 Dominski, Zbigniew, 6075
 Dong, Ke-Wen, 2335
 Donoghue, Daniel J., 1713
 Doppler, Wolfgang, 3745
 Dorai, Thambi, 4165
 Dorée, Marcel, 1171
 Dorfman, David M., 4518
 Dornfeld, Kenneth J., 2013
 Dorsett, Dale, 1894
 Dosaka, Hirotoshi, 6286
 Dotto, G. Paolo, 5364
 Doudna, Jennifer A., 3390
 Douville, Elizabeth M. J., 568
 Downing, James R., 2489
 Dowzer, Celia E. A., 5701
 Draetta, Giulio, 1185, 4253, 6177
 Dretzen, Guy, 523
 Dreyfuss, Gideon, 3419
 Drickamer, Kurt, 1840
 Drouin, Jacques, 3492
 Dubertret, M.-L., 2913
 Dubey, Dharani D., 5346
 Dubin, Robert A., 4340
 Dubois, Evelynne, 2162, 2169, 2852
 Ducommun, Bernard, 6177
 Dueland, Svein, 2049
 Duester, Gregg, 1638
 Dumont, Mark E., 5487
 Dunlap, Jay C., 558
 Dunn, Ashley R., 3399, 4363
 Durvieux, Serge M., 1099
 Dusserre, Yves, 2937
 Dykstra, Christine C., 2576, 2583
 Dymecki, Susan M., 6185
 Earp, H. Shelton, 5016
 Eaton, Suzanne, 5197
 Ebbola, Daniel J., 928
 Eckert, Werner A., 2229
 Eddy, Roger, 1146
 Edgington, Thomas S., 4732
 Edmondson, Diane, 3633
 Edwards, Gwyneth M., 5792
 Edwards, Helen, 2744
 Egan, Sean E., 1344
 Egli, Christoph M., 3060
 Eiden, Maribeth V., 5321
 Eisen, Arri, 1566
 Eisen, Harvey, 2180
 Eisenberg, Marcia T., 894
 Eisenman, Robert N., 5079
 Elgort, Marc, 3868
 Ellis, Christine, 1804, 2018
 Emori, Yasufumi, 344
 Emr, Scott D., 5813
 Eneff, Kenton L., 5206
 Engel, James Douglas, 2778
 Engelke, David R., 721
 Engler, David A., 2425
 Engler, Michael J., 3369
 Epstein, Eileen M., 2282
 Epstein, Lloyd M., 6109
 Erikstein, Bjørn, 3384
 Ernst, Heidemarie, 3735
 Ernst, Matthias, 2503
 Escobedo, Jaime A., 1125
 Espinosa, Rafael, III, 5016
 Esposito, Rochelle Easton, 6306
 Estabrooks, Laurel L., 3711
 Estes, Robert, 1988
 Estridge, J. K., 3925
 Etzold, Thure, 5338
 Evangelista, Carlos C., Jr., 5639
 Evans, Sylvia M., 2273
 Evans, Todd, 843
 Faaland, Carol A., 2697
 Fahrner, Timothy J., 3835
 Falck-Pedersen, Erik, 5977
 Falcone, Domina, 2656
 Falcone, Germana, 3331
 Faller, Douglas V., 3148
 Falzon, Miriam, 117
 Fan, Pang-Dian, 4545
 Fang, Ping, 5090
 Fankhauser, Christian, 2567
 Fanning, Ellen, 5137
 Farina, Antonietta R., 4771

- Farnsworth, Charles L., 4822, 4830
 Faucette, Leo, 1718
 Faust, John B., 4846
 Fazioli, Francesca, 2040, 3191
 Fearon, Eric R., 954
 Feig, Larry A., 4053, 4822, 4830
 Feigenbaum, Lionel, 5479
 Feldhaus, Andrew L., 4885
 Felli, Maria P., 4771
 Felsenfeld, Gary, 843
 Feng, Yue, 2149
 Fenton, Brian, 963
 Feramisco, James R., 1759
 Ferber, Andres, 731
 Ferguson, Kenneth, 1248
 Ferracini, Riccardo, 1793
 Ferrell, James E., Jr., 1965
 Ferris, Douglas K., 1180, 5985
 Fesquet, Didier, 1171
 Field, Jeffrey, 1248
 Fields, Stanley, 5910
 Fikes, John D., 611
 Fink, J. Stephen, 1759
 Finkelman, Fred D., 5660
 Fischberg, Daniel J., 2335
 Fischer, R., 1454, 5068
 Fischer, W. H., 1306
 Fishel, Richard, 2665
 Fisher, Robert C., 1614
 FitzGerald, David, 1751
 FitzGerald, David J., 2200
 FitzGerald, David L., 309
 FitzGerald-Hayes, Molly, 154
 Flavell, David, 4189
 Fleming, J. E., 632
 Fletcher, Bradley, 1754
 Flick, Jeffrey S., 5101
 Florence, Brian, 3613
 Florent, Isabelle C., 2180
 Flores, Osvaldo, 1195
 Foiani, Marco, 3203, 3217
 Fontana, Donna R., 468
 Foote, Simon J., 5244
 Forget, Bernard G., 3528
 Forman, Barry Marc, 5164
 Fornace, Albert J., Jr., 1009
 Forney, James, 1133
 Foster, David A., 102, 4903
 Foulkes, Nicholas, 192
 Fowler, Bruce J., 4732
 Fox, Lyle E., 5275
 Franza, B. Robert, Jr., 1883
 Frati, Luigi, 4771
 Frederickson, Robert M., 2896
 Freeman, Robert S., 1713
 French, Brent A., 2439
 Fresco, Lucille D., 1578
 Freytag, Svend O., 1935, 2291
 Fried, Mike, 1281
 Friedman, Varda, 1372
 Friesel, Robert, 2481
 Fritz, Gerhard, 4660
 Fröhli, Erika, 803
 Frye, Roy A., 5016
 Fu, Ying-Hui, 5735
 Fujioka, Hiroyuki, 2873
 Fukasawa, Kenji, 3472
 Fukui, Yasuhisa, 1207, 1972
 Fukumoto, Yasuo, 2873
 Funderud, Steinar, 3384
 Funk, Walter, 4104
 Furter, Rolf, 4121
 Furter-Graves, Elizabeth M., 4121
 Gaber, Richard F., 4266, 6306, 6317
 Gahl, William, 3676
 Galili, Naomi, 6149
 Gallagher, Patricia M., 5426
 Gallinaro, Hélène, 4581
 Gallo, Gregory J., 281
 Gallwitz, Dieter, 872, 2980
 Gandino, Lucia, 1793, 5954
 Ganguly, Subinay, 3564
 Ganschow, Roger E., 5426
 Garcia, Arnold V., 2273
 Garfinkel, Mark D., 2971
 Garfinkel, Michele, 5497
 Gargano, Silvana, 5624
 Garnier, C., 1114
 Garrett, Stephen, 4045
 Gattoni, Renata, 1258
 Gaughran, Joann P., 3369
 Geddes, Tim J., 2291
 Geiduschek, E. Peter, 5181
 Geiser, Andrew G., 84, 5222
 Geiser, John R., 3842
 Genske, Jane E., 240
 George, Kathleen M., 2778
 Georgel, Philippe, 523
 Gerhart, John C., 1965
 Guerrero, Renee, 1739
 Gerst, Catherine, 1258
 Gerst, Jeffrey E., 1248
 Ghattas, Ingrid R., 5848
 Giangrande, Angela, 523
 Gibbs, Jackson B., 945, 2785, 2812, 3997, 4053
 Gibbs, James S., 4786
 Gibbs, Verna C., 5860
 Gibson, Willie, 894
 Giesman, Donnamarie, 1069
 Gifford, Ann M., 1431
 Giguere, Vincent, 2216
 Gillman, Edwin C., 2382
 Gilmartin, Gregory M., 2432
 Gilmore, Thomas D., 5867
 Gilula, Norton B., 5364
 Gimmi, Edward R., 2324
 Gimpel, Steven D., 3052
 Ginder, Gordon D., 4690
 Ginsberg, Dorit, 582
 Ginsberg, Doron, 582
 Giordano, Silvia, 5954, 6084
 Gishizky, Mikhail L., 854
 Glaser, Tom, 1707
 Glass, James R., 3484
 Glauber, James G., 4690
 Glesne, David A., 5417
 Glimcher, Laurie, 5551
 Godbout, Martin, 3484
 Goebel, Mark, 5767, 5839
 Goeddel, David V., 3454, 5860
 Gojibori, Takashi, 1313
 Goldfarb, Mitchell, 1840
 Goldstein, Samuel, 3905
 Gong, Qi-Hui, 2558
 Gong, Shih S., 6059
 Gonzalez, Frank J., 4927
 Gonzalez, G. A., 1306
 Goodwin, Raymond G., 1590, 3020
 Gopal-Srivastava, Rashmi, 4340
 Gorham, Beverly, 5551
 Gorman, Cornelia, 3070
 Gorovsky, Martin A., 166, 1729, 5410
 Goswami, Shyamal K., 1676
 Gottesdiener, Keith, 2467
 Gottlieb, Roberta A., 2804
 Gourdon, Genevieve, 4679
 Grabowski, Paula J., 5919
 Graf, Thomas, 3987
 Graham, Todd R., 5813
 Gralla, Edith B., 4537
 Gralla, Jay D., 4561
 Granner, Daryl K., 5164
 Grässer, Friedrich A., 3987
 Graves, Joan P., 894
 Gray, Dawn, 1
 Gray, Douglas A., 568
 Gray, Michael W., 2035
 Gray, Patrick W., 5860
 Green, Jeffrey E., 4635
 Green, Peter, 2496
 Greenberg, Arnold H., 1344
 Greenberg, Michael E., 3239, 4545
 Greenfeder, Scott A., 5346
 Gregor, Polly D., 412
 Gregory, Richard J., 3886
 Greider, Carol W., 4572
 Gremke, Linda, 1901
 Grendell, Richard L., 4306
 Griffin, Mary S., 3940
 Grimm, Christian, 289
 Griswold, Michael D., 1448
 Groffen, John, 1180
 Groner, Bernd, 3745
 Gröning, Karsten, 2026
 Gronostajski, Richard M., 2946
 Gros, Philippe, 595
 Grosschedl, Rudolf, 5756
 Grossman, H. Barton, 3699
 Grosveld, Frank, 2216
 Grove, J. Russell, 5541
 Gualdi, Rossana, 6166
 Guarente, Leonard, 611, 4934
 Guerrini, Luisa, 6059
 Guiard, Bernard, 3762
 Guilbaud, Rolande, 202
 Gulino, Alberto, 4771
 Gunderson, Kevin, 3348
 Gunter, Lee E., 2149
 Günzl, Arthur, 5516
 Gupta, D. K., 3879
 Gupta, Shashi, 2026
 Gustafsson, Jan-Åke, 3379, 4314
 Gutkind, J. Silvio, 134, 1500, 3780
 Gutman, Alejandro, 5381
 Habener, Joel F., 2887
 Haber, Daniel A., 1707
 Haber, James E., 5372
 Hagen, David C., 2952
 Hager, Gordon L., 688, 2529
 Hagiwara, Koichi, 2125
 Hagman, James, 5756
 Haguenaier-Tsapis, R., 1114
 Hahn, George M., 6034
 Hahn, William E., 4177
 Hahnenberger, Karen M., 2206
 Hajduk, Stephen L., 1668, 5878
 Halay, Elaine, 108
 Ha Lee, Young M., 1419
 Halegoua, Simon, 4739
 Hall, Benjamin D., 4121
 Halvorsen, Yuan-Di C., 1777
 Hamann, Lutz, 886
 Hamatake, Robert K., 2583
 Hamer, Dean, 3676
 Hamer, Peter, 5867
 Hamlin, J. L., 3850
 Han, Yingshi, 510
 Hanafusa, Hidesaburo, 1207, 1607, 1972
 Handrow, Richard, 3613
 Hanic-Joyce, Pamela J., 2035
 Hannig, Ernest M., 3217
 Hanson, Maureen R., 4274
 Hao, Mingming, 6067
 Hao, Qian-Lin, 1180
 Hapgood, Janet, 4314
 Harada, Hisashi, 3052
 Harashima, Satoshi, 3203, 3229, 3773, 5693
 Harbers, Klaus, 886
 Hardin, Jeff, 1840
 Harding, Heather P., 5005
 Harigaya, Kenichi, 920
 Harlow, Ed, 5792
 Harney, John, 3699
 Harper, David S., 1578
 Harper, Joan E., 5945
 Harpur, Ailsa G., 2057
 Harris, Michael E., 2416, 5878
 Harrison, Charles A., 3735
 Harrison, Stephen, 4207
 Hartung, Stefan, 47, 5154
 Harvey, Richard C., 4846
 Harwood, Janet, 3163
 Hasel, Karl W., 3484
 Hashimoto, Tomoko, 5885, 6041
 Haskell, Kathleen M., 2307
 Hasty, Paul, 4509, 5586
 Hata, Yutaka, 1438
 Hauser, Melinda R., 2425
 Hayashi, Jun, 2697
 Hayashi, Naoyuki, 785
 Hayes, Martha, 4739
 Hayes, Mary K., 5487
 Hazan, Rachel, 913
 Hazel, Thomas G., 3239
 He, Xi, 1739
 Healy, Annette M., 5767
 Hegemann, Johannes H., 3545, 5212
 Heidarani, Mohammad A., 134, 3780
 Heideman, Warren, 4591
 Heino, Jyrki, 972
 Heintz, Nathaniel, 5825
 Heinzel, Scott S., 2263
 Heisterkamp, Nora, 1180
 Hekmatpanah, Daria S., 5781
 Heldin, Carl-Henrik, 2125
 Henderson, Eva, 1734, 2881
 Hendrickson, E. Abner, 3155
 Hermann, Thomas, 4097, 6016
 Herrera, Rafael E., 1270
 Herschman, Harvey R., 1754

- Hershey, John W. B., 3105
 Herskowitz, Ira, 4135
 Heslop, H. E., 1912
 Hickey, Eileen, 544
 Hicks, Geoffrey G., 1344
 Hicks, James B., 2253
 Hickson, Ian D., 1009
 Higashi, Takatsugu, 4088
 Higashio, Kanji, 6041
 Higgs, Douglas R., 4679
 Hildebrandt, John D., 4830
 Hill, Wendy S., 3997
 Himmelspach, Michèle, 1258
 Hinkley, Craig, 641
 Hinnebusch, Alan G., 486,
 2723, 3027, 3203, 3217
 Hino, Masayuki, 5527
 Hipkind, Robert A., 1270
 Hirayoshi, Kazunori, 4036
 Hirose, Fumiko, 4909
 Hisamoto, Naoki, 3317
 Hoffman, Rebecca K., 4473
 Hoffman-Liebermann,
 Barbara, 2375, 4371
 Hoffmann, Birgit, 4097
 Hoffmann, F. Michael, 2319
 Hoffmann, Sylvia, 803
 Hofmann, Annemarie, 2971
 Hogan, Eileen, 5392
 Hohmann, Hans-Peter, 259,
 2315
 Holdridge, Christina, 1894
 Hollenberg, Cornelis P., 5454
 Holmes, Edward W., 5356
 Holmes, Scott G., 5301
 Holt, Jeffrey T., 765
 Holte, Harald, 3384
 Holtzer, Howard, 4473
 Holtzer, Sybil, 4473
 Holtzman, Douglas A., 3399
 Honda, Hiroaki, 2125
 Honegger, A. M., 5068
 Hong, Young S., 3573
 Hopper, Anita K., 2382
 Hopper, James E., 2311
 Hori, Yuichi, 2873
 Horikoshi, Masami, 4809
 Housman, David E., 1707
 Hovanessian, Ara G., 5497
 Howard, Georgette, 4423
 Howe, Philip H., 1185
 Howell, Brian W., 568
 Hsieh, Chih-Lin, 3972
 Hsu, Hai-Ling, 3037
 Hsu, Jui-Chou, 381
 Hsu-Ching, Chen, 4380
 Hu, Guo-Zhen, 4876
 Hu, Qianjin, 5792
 Huang, Haimai, 2075
 Huang, Jin, 3180
 Huang, Manley, 3070
 Huang, Shang-Lang, 2075
 Huberman, Eliezer, 5417
 Huberman, Joel A., 5346
 Hughes, David A., 3088
 Hung, Mien-Chie, 354, 1745,
 1875
 Hunter, Tony, 143, 3682, 4698
 Hüppi, Konrad, 4528
 Hurt, Myra M., 2929
 Hurwitz, Gerard, 2350
 Husmann, Matthias, 4097,
 6016
 Hyman, Linda E., 2004
 Iatrou, Kostas, 1954
 Icely, Pamela L. E., 568
 Iggo, R. D., 1326
 Ihle, James N., 1820, 2391,
 4895
 Imai, Yoshiyuki, 3088
 Immanuel, David, 2133
 Imperiale, Michael J., 1624,
 5977
 Ina, Yasuo, 1313
 Innis, Jeffrey W., 6248
 Innis, Jeffrey W., 5398
 Inoue, Kazushi, 6279
 Irniger, Stefan, 3060
 Ishikawa, Fuyuki, 2125
 Ishiura, Shoichi, 344
 Iwamatsu, Akihiro, 4036
 Iyer, Subramanian V., 4863
 Izaurralde, Elisa, 2567
 Izumi, Tetsuro, 3860
 Jabbar, M. Abdul, 2675
 Jackson, Belinda M., 486
 Jackson, David A., 4405
 Jackson, Jean, 226
 Jackson, Peter, 1107
 Jackson, Stephen P., 2189
 Jacob, Monique, 4581
 Jacquet, Michel, 202
 Jaehning, Judith A., 4555
 Jaenisch, Rudolf, 3070
 Jaenisch, Rudolph, 5154
 Jahn, Carolyn L., 4751
 Jähner, Detlev, 3682
 Jamieson, D. J., 1326
 Jaramillo, Maria, 5992
 Jardine, Karen, 4796
 Jarman, Andrew P., 4679
 Jay, Gilbert, 5222, 5479
 Jaye, M., 5068
 Jeannotte, Lucie, 5578
 Jeanteur, Philippe, 2826, 2832
 Jefferies, David, 338
 Jehn, Birgit, 5212
 Jenkins, Nancy A., 2665,
 3020, 5603
 Jenö, Paul, 27
 Jensen, David E., 4943
 Jerzy, Rita, 1590, 3020
 Jessberger, Rolf, 445
 John, Joseph, 4189
 Johnson, Arlen W., 2593
 Johnson, Daniel E., 4627
 Johnson, Douglas I., 3537
 Johnson, Eric F., 4314
 Johnson, Lee F., 1023
 Johnson, Penny, 1
 Johnson, Randall K., 1718
 Johnston, Gerald C., 5718
 Johnston, Mark, 5101
 Jones, Cheryl, 4207
 Jones, Christopher, 4297
 Jones, Elizabeth W., 5801
 Jones, Raymond E., 2307,
 5792
 Jones, Richard A., 3905
 Jones, Sara, 2641
 Joseph, Cecil K., 102
 Joshi-Barve, Swati, 5435
 Jotte, Robert M., 765
 Jove, Richard, 5059
 Judware, Raymond, 3259
 Jund, R., 1114
 June, Carl H., 3288
 Kabat, David, 4895
 Kabcenell, Alisa K., 2909
 Kadesch, Tom, 6185
 Kadle, R., 363
 Kaibuchi, Kozo, 1438, 2873,
 2909
 Kaina, Bernd, 4660
 Kakunaga, Takeo, 3296, 4088
 Kalberg, Victoria A., 3374
 Kaling, Michael, 93
 Kallin, Bengt, 5338
 Kamada, Shinji, 3296
 Kamata, Nobuyuki, 765
 Kanaan, Moien N., 4356
 Kanda, Naotoshi, 3296
 Kang, Hyun Ah, 3105
 Kang, Lily, 4165
 Kang, Xiaolin, 218
 Kanner, Steven B., 713, 945,
 5113
 Kao, C. Cheng, 63
 Kaplan, David R., 1125
 Karathanasis, Sotirios K.,
 677, 3814
 Karcagi, Veronika, 4128
 Karin, Michael, 2804, 6286
 Karls, Ursula, 886
 Karlsson, Roger, 213
 Kashles, O., 1454
 Kass, Susan, 458
 Kassavetis, George A., 5181
 Katamine, Shigeru, 1500
 Kato, Gregory J., 954
 Kato, K., 1523
 Kato, Shingo, 920
 Katsumata, Makoto, 3786
 Katz, Wendy S., 4726
 Katzav, S., 1912
 Katze, Michael G., 5497
 Katzen, Alisa L., 226
 Kauffman, Michael G., 2538
 Kaufmann, William K., 3711
 Kaulen, Hildegard, 412
 Kavanaugh, W. Michael, 1125
 Kawasaki, Hiroshi, 344
 Keeble, Winifred W., 2547
 Keene, Jack D., 1578, 1829
 Keene, Richard G., 4599
 Kellems, Rodney E., 5398,
 6248
 Keller, L. R., 2328
 Kelliher, Michelle, 4710
 Kelly, Joan M., 5701
 Kelly, Thomas J., 2108, 2538
 Kemp, David J., 5244
 Kempler, Geraldine, 1214
 Kenter, Amy L., 4398
 Kere, Juha, 4015
 Kern, Michael J., 578
 Kerr, Ian M., 4189
 Kerr, Niall C. K., 1009
 Keys, Robert D., 3997
 Khan, C. M. Anjam, 963
 Kiefer, Paul, 5929
 Kiessling, Ann A., 5190
 Kiledjian, Megerditch, 6185
 Kilpatrick, Jay E., 1624
 Kim, Hyung-Suk, 2769
 Kim, Jae-Hong, 3894
 Kim, Kyung Young, 5222
 Kim, Seong-Jin, 84, 5222
 Kim, Uh-Hyun, 2040
 Kim, Yong Kyu, 2296
 Kimura, Shioiko, 4927
 Kingston, Robert E., 281
 Kinoshita, Noriyuki, 5839
 Kinzler, Kenneth W., 1724
 Kirkegaard, Karla, 3719
 Kirkpatrick, David, 5801
 Kirsch, Ilan R., 5462
 Kishi, Kiyohiko, 2873
 Kister, Liliane, 4581
 Kitada, Kunio, 2583
 Kitch, Barry, 5016
 Klein, John R., 5902
 Klemenz, Roman, 803
 Knipe, David M., 4786
 Knippers, Rolf, 6257
 Knopf, John, 2018
 Knott, Amy, 4710
 Knox, Jennifer J., 2946
 Ko, Christopher H., 4266
 Ko, Linda J., 2778
 Kohalmi, Lester, 218
 Kohda, Takashi, 3522
 Kohli, Jürg, 289
 Kolb, Janet M., 746
 Kolbeck, Roland, 2315
 Kole, Ryszard, 6075
 Kolodner, Richard D., 2593
 Kolodziej, Peter A., 4669
 Koltin, Yigal, 1718
 Konieczny, Stephen F., 267
 Koo, Jah-Won, 1980
 Kornberg, Thomas, 226
 Korner, Mira, 1017
 Koser, Paul L., 1718
 Koshland, Douglas, 5592
 Koudou, Sophia, 677
 Kovary, Karla, 2451, 4466,
 5470
 Kozak, Leslie P., 4147
 Kraal, Georg, 1176
 Krangel, Michael S., 5671
 Krauskopf, Anat, 1195, 3515
 Krauss, Robert S., 3915
 Krikau, Mark F., 4751
 Krude, Torsten, 6257
 Krueger, David A., 4157
 Krug, Robert M., 1092
 Kruger, Warren, 4135
 Kruijer, Wiebe, 192
 Krysan, Patrick J., 1464, 2263
 Kubelik, Anne R., 4022
 Kudo, Hitoshi, 4036
 Kuff, Edward L., 117
 Kugler, Wilfried, 93
 Kuhn, Rainer, 4642
 Kumar, Ashok, 1676
 Kumar, Nalin M., 5364
 Kumar, Rakesh, 979
 Kundu, Amitabha, 2675
 Kunz, Bernard A., 218
 Kuo, Frank C., 6050
 Kuo, Hai-Chien, 5919
 Kurban, R. R., 2057
 Kurjan, Janet, 4196
 Kurokawa, Kiyoshi, 3296
 Kusakari, Satoshi, 920
 Kuter, David J., 6116
 La Bella, Franca, 5825
 Lacal, Pedro, 1500

- Lacroute, François, 3075
 Lader, Eric, 6197
 Ladias, John A. A., 677
 Laemmli, Ulrich K., 2567
 Lafyatis, Robert, 3795
 Lai, Susan T., 2236
 Laiho, Marikki, 972, 4952
 L'Allemain, Gilles, 1002
 Lambowitz, Alan M., 1696, 4022
 Landau, Nathaniel R., 1785, 5229
 Landfear, Scott M., 240
 Landick, Robert, 4599
 Landsman, David, 4483
 Lane, D. P., 1326
 Lang, B. Franz, 5746
 Laski, Frank A., 1538
 Laskin, Jeffrey D., 2697
 Latchman, D. S., 3925
 La Thangue, N. B., 1686
 Lau, Lester F., 2804, 3239
 Laughon, Allen, 3613
 Laursen, Richard A., 5867
 Laz, Thomas M., 381, 1393
 Lazar, Mitchell A., 5005
 Lazarow, Paul B., 510
 Lazo, Pedro A., 2864
 Lazo, Pedro S., 5470
 Lea, Kristi, 4651
 Le Beau, Michelle M., 5016
 Lebleu, Bernard, 2832
 Le Bouffant, Françoise, 1171
 Lechleider, Robert, 3795
 Lee, Amy S., 2296, 3446, 5612
 Lee, Angela L., 4306
 Lee, Christine S. L., 5032
 Lee, Frances, 5562
 Lee, Hy-De, 5222
 Lee, Insong J., 1048
 Lee, Jae-Yong, 721
 Lee, Kevin A. W., 4297
 Lee, M. G.-S., 2467
 Lee, S. C., 4959
 Lee, Te-Chung, 5090
 Lefebvre, Philippe, 2529
 Le Guellec, René, 3395
 Lehmann, Jürgen, 4097
 Leighton, John K., 2049
 LeMagueresse, Brigitte, 3960
 Lemaigre, Frédéric P., 1099
 Lemansky, P., 3879
 Lemke, Greg, 4642
 Lennard, Andrew S., 1281
 Leof, Edward B., 1185
 Leon, Patricia, 533
 Leonard, J., 1306
 Leonard, Mark W., 2778, 6128
 Leone, Sandra, 3171
 Lepesant, J.-A., 2913
 Le-Roscouet, Danièle, 202
 Leshkowitz, Dena, 1547
 Leslie, Kevin B., 5562
 LeStourgeon, Wallace M., 864
 Letwin, Kenneth, 2496
 Levy, Joan B., 4165
 Levy, Mark A., 1718
 Lew, Daniel J., 182, 5147
 Lew, John, 568
 Lewis, Deborah A., 3804
 Ley, Timothy J., 1500
 Lhoták, Vladimír, 2496
 Li, Dawei, 1023
 Li, Li, 3633
 Li, Li-Jing, 5612
 Li, Suzanne C., 5551
 Li, W., 5068
 Li, Wei, 3756
 Li, Wen-Zhuo, 666
 Li, Xuan, 3446
 Li, Yuchi, 1883
 Li, Yue, 1023
 Liang, Li-Fang, 6197
 Liao, Xinheng, 38
 Lickteig, Ronald L., 1988
 Lieber, Michael R., 3972
 Lieberman, Paul M., 63
 Liebermann, Dan A., 2375, 4371
 Liebert, Monica, 3699
 Liebhaver, Stephen A., 3786
 Lillycrop, K. A., 3925
 Lin, Chien R., 1739
 Lin, Haishan, 267
 Lin, Lih-Ling, 2018
 Lin, Ren-Jang, 5571
 Lin, Zhongxiang, 4473
 Lin-Chao, Sue, 2075
 Lindberg, Richard A., 143
 Linder, Patrick, 3463
 Lindquist, Susan, 1062
 Lindsten, Tullia, 3288
 Link, Daniel C., 1500
 Linn, Stephen C., 1508
 Lipke, Peter N., 4196
 Lipsick, Joseph S., 3987
 Lis, John T., 5285
 Liska, DeAnn J., 2066
 Liskay, R. Michael, 4839
 Little, Jane A., 4690
 Littman, Dan R., 1785, 5506
 Liu, Edison T., 5016
 Liu, Jen-Kuei, 773
 Liu, Qiurong, 1531
 Liu, Vivian F., 3155
 Liu, Zingquan, 2511
 Livi, George P., 1718
 Livingston, David M., 972
 Livingston, Dennis M., 2013
 Livneh, Etta, 126
 Lo, Kiersten, 5229
 Lock, Peter, 3399, 4363
 Lodi, Tiziana, 3762
 Lodish, Harvey F., 1980
 Lombardi, Daniela, 134, 3780
 Lombardi, Donald P., 5462
 Lonardo, Fulvio, 3191
 London, Lucille, 4599
 Long, Roy M., 2311
 Longati, Paola, 1793, 5954
 Lorca, Thierry, 1791
 Lord, Kenneth A., 4371
 Loros, Jennifer J., 558
 Lowe, David G., 3454
 Lowy, Douglas R., 2819, 3132, 6026
 Lozano, Guillermina, 6067
 Lu, Cha Fen, 4196
 Lu, John, 4627
 Lucas, Peter C., 5164
 Ludlow, John W., 972
 Luetke, Karen, 4497
 Luk, Daniel, 3624
 Lukash, Lubov, 1927
 Lumelsky, Na'ya L., 3528
 Lumpkin, Charles K., 1372
 Lund, S. Diane, 5426
 Luo, Chunsheng, 468
 Luo, Yan, 3660
 Luo, Ying, 5291
 Lupton, Stephen D., 3374
 Luse, Donald S., 1508
 Lyman, Stewart D., 3043
 Lynch, David, 1590
 Ma, Averil, 440
 Ma, Qiufu, 1754
 MacArthur, Linda, 5321
 Mackman, Nigel, 4732
 Macleod, Kay, 4324
 MacNeill, S. A., 1326
 Mader, Sylvie, 3247
 Magasanik, Boris, 822, 4455, 6216, 6229
 Mahdavi, Vijak, 3814
 Maher, Veronica M., 1927
 Majors, John, 564
 Majors, John E., 5848
 Mäkelä, Tomi P., 4015
 Maley, Stephen, 4207
 Maller, James L., 3860
 Malone, Elizabeth A., 3009, 5710
 Mamon, Harvey J., 2794
 Manabe, Yoshihisa, 3296
 Manak, J. Robert, 3652
 Manavalan, Parthasarathy, 3886
 Maniatis, Tom, 1239
 Manley, James L., 5945
 Manolson, Morris F., 5801
 Manoukian, Armen, 2946
 Manzella, Livia, 6166
 Marcus, Stevan, 1030, 3603
 Marczak, Judith E., 2609
 Maresca, Bruno, 5624
 Marini, Nicholas J., 299
 Maroder, Marella, 4771
 Marshall, Margaret A., 55
 Marshall, Mark S., 3997
 Martin, G. Steven, 1965
 Martin, Nancy C., 1662, 2382
 Martin, Patrick, 3132
 Martin, Sandra L., 4804
 Martinez, Ernest, 2937
 Martinotti, Stefano, 4771
 Marykwas, Donna L., 4196
 Maryon, Ed, 3268, 3278
 Marzluf, George A., 4356, 5735
 Marzluff, William F., 497, 2416, 2929
 Mascareno, Eduardo, 1676
 Maschat, F., 2913
 Massague, Joan, 4952
 Massagué, Joan, 972
 Masuoka, Howard, 1734, 2881
 Mathews, Christopher K., 20
 Matsuda, Michiyuki, 1607
 Matsuda, Satoru, 833
 Matsui, Toshimitsu, 134
 Matsukage, Akio, 4909
 Matsumoto, Yoshihiro, 4441
 Matsumoto, Yutaka, 2905
 Mattox, Paul A., 2547
 Matunis, Erika L., 3419
 Mayer, Bruce J., 1607
 Mayer, Stephen A., 813
 McAlister-Henn, Lee, 370
 McAvoy, Elizabeth M., 2307
 McBride, Jana S., 963
 McBride, M. Scott, 1638
 McBride, O. Wesley, 1009
 McBurney, Michael W., 4796
 McCaffrey, Gretchen, 2952
 McCarthy, Thomas L., 250, 4490
 McCloskey, R. Patrick, 3972
 McClung, J. Keith, 1372
 McCormick, F., 1523
 McCormick, Frank, 1804
 McCormick, J. Justin, 1927
 McCusker, John H., 746
 McDonnell, Donald P., 4350
 McEwen, Joan E., 2399
 McEwen, Stephen, 3399
 McGregor, W. Glenn, 1927
 McIntosh, Evan M., 329
 McKendry, Roslyn, 4189
 McLaughlin, Jami, 4710
 McMahon, Martin, 4760
 McNally, Francis J., 5648
 McPheat, J., 1326
 McWhirter, John R., 1553
 Means, Anthony R., 3960
 Méchali, Marcel, 655
 Mecht, Nadir, 2832
 Meco, Daniela, 4771
 Medcalf, Elizabeth A., 12
 Medema, René H., 5963
 Meeker, Timothy C., 4846
 Meinkoth, Judy L., 1759
 Meisler, Arnold I., 3842
 Meisler, Miriam H., 4423
 Meister, Andreas, 4985
 Melby, Anna E., 381, 1393
 Melnyk, Ostap, 4846
 Mendelsohn, John, 979
 Menold, Marisa M., 4045
 Menzel, P., 1306
 Meola, Giovanni, 2236
 Mercer, W. Edward, 731
 Merchant, Juanita L., 2686
 Mermelstein, Fred H., 2697
 Mermod, Nicolas, 2937
 Merrell, Kevin T., 1765
 Merrick, William C., 5992
 Merrill, Gary F., 3726
 Messenguy, Francine, 2162, 2169, 2852
 Mestrl, Ruben, 5937
 Meurs, Eliane, 5497
 Meuth, Mark, 3163
 Meyale, S., 3879
 Meyer, Barbara E., 4739
 Meyer, Jutta, 5454
 Meyer, Sylvie, 4581
 Meyerowitz, Elliot M., 2971
 Michael-Michalovitz, Dan, 582
 Middlemas, David S., 143
 Mielenz, Jonathan, 4333
 Miki, Toru, 1500
 Milbrandt, Jeffrey, 3835
 Miller, Sarah E., 6197
 Miller, Carla, 3842
 Miller, Cheryl L., 4885
 Miller, David, 3603
 Miller, Donald M., 2154
 Miller, Kenton S., 5902
 Miller, Paul F., 486
 Miller, Rehae C., 6337

- Miller, Stephen M., 4455, 6229
 Milner, Jo, 12
 Minard, Karyl I., 370
 Minchiotti, Gabriella, 5171, 5624
 Minehart, Patricia L., 6216
 Mineo, Ikuro, 5356
 Miner, Jeffrey H., 2842
 Minvielle-Sebastia, Lionel, 3075
 Misawa, Yukiko, 5527
 Misra, Ravi, 3239
 Misra, Ravi P., 4545
 Mitra, Sankar, 4660
 Mittman, Barbara A., 4111
 Mitts, Marjane R., 4591
 Miura, Osamu, 4895
 Miura, Shigeto, 1313
 Miwa, Takeshi, 3296
 Miyake, Sanae, 3088
 Miyao, Yasuyoshi, 5885
 Miyatake, Shoichi, 5894
 Miyazono, Kohei, 2125
 Miyoshi, Jun, 4088
 Mizuno, Kimio, 4927
 Mizuno, Takakazu, 2873
 Moehle, Charles M., 2723
 Moerman, Elena J., 3905
 Mohammadi, M., 5068
 Mohn, Kenneth L., 381, 1393
 Molloy, Christopher J., 2040
 Molony, Lisa A., 721
 Mondino, Anna, 6084
 Monica, Katherine, 6149
 Montarras, Didier, 226
 Monteagudo, M. Cristina, 5592
 Montine, Kathleen S., 2896
 Montminy, M. R., 1306
 Montminy, Marc R., 1759
 Monuki, Edwin S., 4642
 Moore, Claire L., 2004
 Moore, Paul A., 5330
 Mooslehner, Katrin, 886
 Moraes, Carlos T., 1631
 Moran, Elizabeth, 2116, 4253, 5389
 Moran, Michael F., 1804
 Morand, Janice, 1133
 Morgan, Brian A., 4111
 Morgan, William D., 3504
 Morgenbesser, Sharon D., 6007
 Morii, Hiroto, 5527
 Morimoto, Richard I., 586
 Morinaga, Tomonori, 6041
 Moritz, Michelle, 5681
 Moritz, Robert L., 803
 Morris, Timothy D., 544
 Morrissey, Louisa M., 3719
 Moscona, A. A., 5275
 Mosialos, George, 5867
 Mosley, R. Lee, 5902
 Moss, Jennifer, 3949
 Moss, Joel, 1146
 Mosser, Scott D., 3997
 Mountz, John D., 5660
 Mowat, Michael, 1, 1344
 Mukai, Hiroyuki, 4088
 Mukai, Yukio, 3773
 Mulder, Maarten, 192
 Mullenders, Leon H. F., 4128
 Muller, Alexander J., 1785
 Müller, Ursula, 886
 Mulligan, R. Michael, 533, 4278
 Mumby, Marc, 4282
 Mumby, Marc C., 1988, 1996
 Mun, Byung-Joo, 20
 Mundscha, Laura J., 3148
 Munn, Alan L., 3868
 Munz, Peter, 289
 Murano, Shunichi, 3905
 Murray, Edward J., 5534
 Murre, Cornelis, 1156
 Murtagh, James J., Jr., 1146
 Musgrove, Elizabeth A., 5032
 Mushinski, J. Frederic, 3095, 5660
 Mylin, Lawrence M., 2311
 Nadal-Ginard, Bernardo, 3814
 Nagata, Kazuhiro, 4036
 Naidner, Fred, 1030, 3603
 Nakabayashi, Hidekazu, 5885
 Nakai, Akira, 4036
 Nakajima, Koichi, 1409
 Nakamura, Masataka, 1313
 Nakamura, Yasuhara, 3317
 Nakano, Akihiko, 5727
 Nakazawa, Nobushige, 5693
 Naldini, Luigi, 1793
 Namba, Yujiro, 833
 Namen, Anthony E., 1590
 Nandabalan, Krishnan, 1777
 Nash, Theodore E., 3326
 Nasheuer, Heinz-Peter, 2081
 Nasim, Faiz-ul H., 5919
 Natarajan, A. T., 4128
 Naujokas, Monica A., 2962
 Navarro, David, 5612
 Nawaz, Zafar, 4350
 Nayak, Debi P., 2675
 Neckers, Leonard M., 1360
 Needleman, David S., 3960
 Negreanu, Varda, 554
 Nehlin, Jan Olof, 4876
 Nehls, Michael C., 4065
 Nelson, Joanne O., 4415
 Neubauer, Andreas, 5016
 Nevins, Joseph R., 2432
 Newlon, Carol S., 5346
 Nicholson, B. J., 363
 Nicolaides, Nicholas C., 6166
 Niedenthal, Rainer, 3545, 5212
 Niedzwiecki, A., 632
 Niki, Masaru, 1313
 Nishida, Yasuyoshi, 4909
 Nishikawa, Shuh-Ichi, 5727
 Nishimoto, Takeharu, 3317
 Nishimura, Mamoru, 3229
 Niyogi, Salil K., 2425
 Noguchi, Tetsuro, 5470
 Nohiro, Yukiko, 3317
 Nomura, Masayasu, 746, 754
 Nordheim, Alfred, 1270
 Nori, Mukund, 2812
 Nourse, Jamison, 6149
 Novick, Peter J., 2909
 Nuell, Mark J., 1372
 Numata, Noboru, 1313
 Nuoffer, Claude, 27
 O'Brien, Jeanne M., 3537
 O'Brien, Melanie C., 1207, 5059
 O'Brien, Thomas, 5285
 O'Bryan, John P., 5016
 O'Connell, Peter, 906
 O'Connor, J. Patrick, 425
 Ohbo, Kazuyuki, 1313
 Ohtani, Kiyoshi, 1313
 Ohuchi, Tooru, 4088
 Oishi, Michio, 3522
 Okayama, Hiroto, 5321
 Okazaki, Kenji, 4528
 Oketani, Makoto, 75
 Olesen, James T., 611
 Oliff, Allen, 2307
 Oliver, Stephen G., 4235
 Olson, Eric N., 2439, 3633, 4854, 6103
 Olwin, Bradley B., 2319
 O'Malley, Bert W., 4350, 4998
 Ong, Loke Y., 5346
 Ono, Tomio, 3960
 Oren, Moshe, 582
 Organ, Edward L., 2149
 Orkin, Stuart H., 4518
 Osborn, Kathy, 1023
 Osborne, H. B., 3115
 Osheim, Yvonne N., 3823
 Oshima, Yasuji, 785, 3229, 3773, 5693
 Oskarsson, Marianne, 604
 Ossig, Rainer, 872, 2980
 Ostermeyer, Elizabeth, 3171
 Ouellette, Laurie A., 3537
 Overell, Robert W., 1590, 3374
 Owens, Garrison A., 1372
 Owens, Gregory P., 4177
 Owens, James D., Jr., 5660
 Ozenberger, Bradley A., 1222
 Pabon-Pena, Lil M., 6109
 Paciucci, Rosanna, 1334
 Paddon, Christopher J., 3203
 Pal, Subrata K., 5190
 Palfi, Zsolt, 2026, 5516
 Paluh, Janet L., 928, 935
 Pandey, Niranjan B., 497
 Papageorge, Alex G., 3132, 6026
 Papathanasiou, Mathilda A., 1009
 Parent, Stephen A., 4616
 Pari, Giovanna, 4796
 Paris, J., 3115
 Paris, Jeannie, 3395
 Park, Linda S., 3052
 Park, Morag, 2962
 Park, Ronald E., 1739
 Parsons, J. Thomas, 713, 945, 5113, 5832
 Parsons, Janey N., 4074
 Pastan, Ira, 1751, 2200
 Patel, Pragna I., 4157
 Patient, Roger K., 6128
 Patterson, Catherine E., 4717
 Patton, Jeffrey R., 5998
 Paul, Sucharita, 3886
 Novick, Peter J., 2909
 Nuell, Mark J., 1372
 Numata, Noboru, 1313
 Nuoffer, Claude, 27
 O'Brien, Jeanne M., 3537
 O'Brien, Melanie C., 1207, 5059
 Pabon-Pena, Lil M., 6109
 Paciucci, Rosanna, 1334
 Paddon, Christopher J., 3203
 Pal, Subrata K., 5190
 Palfi, Zsolt, 2026, 5516
 Paluh, Janet L., 928, 935
 Pandey, Niranjan B., 497
 Papageorge, Alex G., 3132, 6026
 Papathanasiou, Mathilda A., 1009
 Parent, Stephen A., 4616
 Pari, Giovanna, 4796
 Paris, J., 3115
 Paris, Jeannie, 3395
 Park, Linda S., 3052
 Park, Morag, 2962
 Park, Ronald E., 1739
 Parsons, J. Thomas, 713, 945, 5113, 5832
 Parsons, Janey N., 4074
 Pastan, Ira, 1751, 2200
 Patel, Pragna I., 4157
 Patient, Roger K., 6128
 Patterson, Catherine E., 4717
 Patton, Jeffrey R., 5998
 Paul, Sucharita, 3886
 Novick, Peter J., 2909
 Nuell, Mark J., 1372
 Numata, Noboru, 1313
 Nuoffer, Claude, 27
 O'Brien, Jeanne M., 3537
 O'Brien, Melanie C., 1207, 5059
 Pays, Etienne, 338
 Pays, Etienne, 1473
 Pearson, Barbara E., 2081
 Pecorino, Lauren T., 3139
 Peebles, Craig L., 425
 Pei, Duanqing, 1480
 Pelech, Steven, 2517
 Pellegrini, Sandra, 4189
 Pelletier, Jerry, 1707
 Pellicer, Angel, 1334
 Pendergast, Ann-Marie, 1785
 Pennica, Diane, 5860
 Pepin, Marie-Claude, 1647
 Pereira, Lenore, 5612
 Perkins, Archibald S., 2665
 Perlmann, Thomas, 5259
 Perry, Michael, 641
 Perry, Robert P., 2324
 Peters, Gordon, 5929
 Petersen, Richard, 1214
 Peterson, Martha L., 2324
 Petes, Thomas D., 737
 Petralia, Salvatore, 731
 Petrangeli, Elisa, 4771
 Petryniak, Bronislawa, 3288
 Petryshyn, Raymond, 3259
 Pfahl, Magnus, 4097, 6016
 Pfeffer, Lawrence M., 4903
 Pfohl, Jeffrey L., 5671
 Philippe, M., 3115
 Philippe, Michel, 3395
 Philipson, Lennart, 5338
 Phillips, Benette, 586
 Phillips, John C., 468
 Phizicky, Eric M., 5410
 Piatigorsky, Joram, 1488, 4340
 Picataggio, Stephen, 4333
 Piechaczyk, Marc, 2832
 Pierce, Jacalyn H., 134, 3191, 3780
 Pierce, Jacqueline W., 1431
 Pingel, Jeanette T., 4415
 Pipas, James M., 2116, 3842
 Pittelkow, Mark R., 2547
 Plamann, Michael, 928
 Plass, Christoph, 2229
 Pleiman, Christopher M., 3052
 Plowman, Gregory D., 2547
 Plumb, Mark, 4324
 Poellinger, Lorenz, 401, 3379, 4314
 Pognonec, Philippe, 412, 5125
 Pogue-Geile, Kay, 3842
 Pogulis, Robert J., 2291
 Polakis, Paul, 1804
 Pollack, Robert E., 3472
 Pollard, Victoria W., 1668
 Pondel, Mark, 1785
 Pongratz, Ingemar, 4314
 Pongubala, Jagan M. R., 1040
 Poon, David, 4809
 Popoff, Sonya C., 4537
 Porter, Stephen C., 5426
 Posada, James, 2517
 Potter, Michael, 3095
 Powers, Scott, 3894
 Praitis, Vida, 4726
 Prat, Maria, 1793, 5954
 Prats, Hervé, 573
 Preston, Robert A., 5801
 Price, Brendan D., 3365
 Price, Daniel J., 5541
 Pringle, John R., 1295, 5767

- Prochownik, Edward V., 3699
 Prokop, Carol, 5016
 Pruitt, Kim D., 4274
 Prywes, Ron, 3652
 Pu, William T., 4918
 Puetz, John J., 3835
 Pulaski, Beth A., 5681
 Pulido, D., 1912
- Qadri, Ishtiaq, 5612
 Qian, Zuwei, 5312
 Qiu, Hong Fang, 2169
 Quilliam, L. A., 1523
 Qureshi, Sajjad A., 102
- Radany, Eric, 3972
 Radzioch, Danuta, 2718
 Raibaud, Anna, 2180
 Rall, Thomas B., 4448
 Ralph, David A., 4952
 Ralph, Stephen, 3399, 4363
 Ralph, Stephen J., 2057
 Ramain, Philippe, 523
 Ramamurthy, Lakshman, 2416
 Ramirez, Manuel, 3027
 Ramotar, Dindial, 4537
 Ramsay, Robert, 4363
 Rapatz, Winfried, 699
 Rapp, Ulf, 913
 Ratajczak, T., 4959
 Rath, Asha, 3339
 Rattner, Amir, 1017
 Ravid, Katya, 6116
 Ray, Bryan L., 5372
 Ray, Ratna, 2154
 Raycroft, Loretta, 6067
 Rebstein, Patrick J., 2946
 Reddy, Ram, 5266
 Redford, Peter, 2819
 Redondo, Juan Miguel, 5671
 Reedijk, Michael, 3043
 Reid, Laura H., 2769
 Reid, Lola M., 108
 Reinberg, Danny, 1195
 Reis, Robert J. Shmookler, 3905
 Reiss, Krzysztof, 731
 Remy, Roland, 259, 2315
 Repetto, Barbara, 3931
 Resar, Linda M. S., 954
 Reveillaud, I., 632
 Reyes, Antonio A., 1654
 Reynolds, Albert B., 713, 5113, 5832
 Rhee, Sue Goo, 2040
 Rhoads, Robert E., 5435
 Rhodes, Linda, 5639
 Rhodes, Linda D., 4885
 Ricciardi, Robert P., 4287
 Rice, Glenn, 5860
 Rich, Devra P., 3886
 Richards, Frank F., 6139
 Richards, Geoff, 523
 Ridley, P. ob, 963
 Riezman, Howard, 27, 5251
 Rigby, Peter W. J., 5534
 Riggs, Karen J., 1765
 Riggs, Michael, 3554
 Rincón-Limas, Diego E., 4157
 Rine, Jasper, 1080, 5648
 Ringold, G. M., 4959
 Rinker-Schaeffer, Carrie, 5435
 Rippe, Richard A., 4065
 Rivera, Victor M., 4545
- Rivera-Pérez, Jaime, 4509, 5586
 Rivier, David H., 1382
 Rizzo, Cheryl A., 5470
 Ro, Hyo-Sung, 2303
 Robbins, Jay H., 1009
 Robbins, Keith C., 1500
 Roberts, Anita B., 84, 3795, 5222
 Roberts, Thomas M., 2794
 Robertson, Elizabeth J., 5578
 Robinson, Gordon W., 620
 Robinson, Jane S., 5813
 Robinson, Jane V., 963
 Roca, Herman, 4497
 Rodan, Gideon A., 2503
 Rodgers, Linda, 3554
 Rodkey, Karyn, 1133
 Rodrigues, Gerard A., 2962
 Rodriguez, Marianne, 4244
 Roeder, G. Shirleen, 1222
 Roeder, Robert G., 412, 4809, 5125
 Roghi, Christian, 3395
 Rohlman, Christopher E., 721
 Rollins, Barrett J., 3125
 Romeo, Annette M., 2253
 Ron, David, 2887
 Roncari, Daniel A. K., 2303
 Ronne, Hans, 4876
 Rönstrand, Lars, 972
 Rooney, John W., 4885
 Rosen, Haim, 1017
 Rosen, Ora M., 3407
 Rosenberg, Naomi, 440, 4710
 Rosenberg, Richard K., 6286
 Rosenberg, Robert D., 6116
 Rosenblum-Vos, Lynne S., 5639
 Rosenfeld, Michael G., 1739
 Rosenthal, Nadia, 3735
 Rosolen, Angelo, 1360
 Ross, Janet, 1883
 Ross, Katrin, 93
 Ross, Robert S., 2273
 Roth, H. John, 1488
 Rothman, Paul, 5551
 Rotin, D., 5068
 Rottapel, Robert, 3043
 Rottman, Jeffrey N., 3814
 Roudebush, Margaret, 2785
 Rousseau, Guy G., 1099
 Rowley, Adele, 5718
 Roy, Amit, 4196
 Rubinstein, M., 5068
 Rudolph, Karen, 1846
 Ruediger, Ralf, 4282
 Ruggiero, Marco, 134, 3780
 Ruis, Helmut, 699
 Ruiz, Joseph C., 5578
 Rundell, Kathleen, 1988, 1996
 Runge, Kurt W., 2919
 Runkel, Laura, 1270
 Ruoqian-Shen, 1676
 Ruppert, J. Michael, 1724
 Rutter, William J., 4985
 Ryffel, Gerhart U., 93
- Sachs, Leo, 554
 Sachs, Matthew S., 928
 Sadowski, Paul D., 4497
 Saffer, Jeffrey D., 2189
 Sagliocco, Francis A., 5330
- Sahlén, Pelle, 2125
 Saito, Toshiyuki, 833
 Sakano, Hitoshi, 4528
 Sakoulas, George, 3472
 Saltman, David, 6149
 Salton, Stephen R. J., 2335
 Samad, Akhtar, 1598
 Samuels, Herbert H., 5164
 Samuels, Mark E., 3584
 Samuelson, Linda C., 4423
 Sanes, Joshua R., 5848
 Sanghera, Jasbinder, 2517
 Santoro, Irma M., 1944, 6296
 Sasaki, Takuya, 1438, 2909
 Sassone-Corsi, Paolo, 192
 Sawada, Shinichiro, 5506
 Scaife, John G., 963
 Scarlato, Guglielmo, 2236
 Scarpulla, Richard C., 5631
 Scazzocchio, Claudio, 795, 5746
 Schaack, Jerome, 3355
 Schaefer, Frederick V., 5902
 Schaer, Primo, 289
 Schäfer, Reinhold, 803
 Schatzle, John, 3339
 Schatzman, Randall C., 4760
 Schedl, Paul, 3584, 4973
 Scheidreith, Claus, 259
 Scheidtmann, Karl Heinz, 1996
 Schekman, Randy, 5727
 Scheppeler, Judith A., 1883
 Schildkraut, Carl L., 6268
 Schiller, John T., 6026
 Schimmel, Paul, 2744
 Schlessinger, J., 1454, 5068
 Schlessinger, Joseph, 913, 3756
 Schmid, Stefanie R., 3463
 Schmidt, Edward E., 3726
 Schmidt, Juliann R., 6067
 Schmidt, Martin C., 63
 Schmierer, Ann, 1590
 Schmitt, Hans Dieter, 872, 2980
 Schmitt-Ney, Michael, 3745
 Schneider, Edward L., 1372
 Schneider, Jane C., 4934
 Schneiderman, Martin H., 2416
 Schnier, Joachim, 3105
 Schon, Eric A., 1631
 Schrader, John W., 2901, 5562
 Schreiber, Robert D., 5860
 Schroeder, Stephanie, 4809
 Schuetz, Thomas J., 281
 Schuh, Susan M., 5985
 Schulman, Ira G., 166
 Schulte, Ulrich, 1696
 Schultes, Neil P., 322
 Schultz, Joshua R., 1901, 6337
 Schümperli, Daniel, 2416
 Schwartz, Robert J., 2439, 5090
 Schwelberger, Hubert G., 3105
 Scolnick, Edward M., 3997
 Scorsone, Kathleen, 1745
 Screpani, Isabella, 4771
 Seal, Samarendra N., 2704
 Seal, Samar N., 4863
 Segatto, Oreste, 2040, 3191
- Seiler, Stephanie H., 2004
 Sekiguchi, Takeshi, 3317
 Selman, Bruce R., 5053
 Seo, Yeon Soo, 2350
 Sethi, Neerja, 5592
 Setzer, David R., 3978
 Shacter, Emily, 3095
 Shah, Neil P., 1854
 Shahan, Karen, 4244
 Shanske, Sara, 1631
 Sharpe, Jacqueline A., 4679
 Shaw, Peter E., 1270
 Shean, Mary Lou, 1638
 Shen, Chun-Pyn, 6185
 Shen, Minhua, 1813
 Shenk, Thomas, 3355
 Shenkar, Robert, 1813
 Shepard, H. Michael, 979
 Sherman, Fred, 666, 5487
 Sherr, Charles J., 2489
 Shesely, Edward G., 2769
 Shibuya, Masabumi, 5527
 Shih, Chiao, 1480
 Shim, Yhong Hee, 4651
 Shio, Helen, 510
 Shiozaki, Kazuhiro, 6093
 Shipley, Gary D., 2547
 Shirakata, Masaki, 4528
 Shiu, Esther C., 6034
 Shivji, M. K. K., 1686
 Shlomal, Joseph, 5894
 Shore, David, 3642
 Shows, Thomas B., 1146
 Shoyab, Mohammed, 2547
 Shtivelman, Emma, 5446
 Shu, Hsiao-Hsueh, 1662
 Shu, Min, 3842
 Shurtleff, Sheila A., 2489
 Sibley, Carol Hopkins, 4885
 Siddiqui, M. A. Q., 1676
 Sieber, Jennifer, 737
 Siegal, Clay B., 1751
 Sikorska, Marianna, 2752
 Silar, Philippe, 1232
 Silve, S., 1114
 Silveira, Linda, 3868
 Simburger, Kelli S., 3835
 Simmons, Donna M., 1739
 Simon, Manuel, 699
 Simpson, Richard J., 803
 Singer, Dinah S., 4217, 4228
 Singer, Richard A., 5718
 Singh, Harinder, 4885
 Singh, N., 391, 2362
 Singleton, D., 2362
 Sizeland, Andrew M., 4005
 Skalniak, David G., 4518
 Skeiky, Yasir A. W., 1954
 Sklar, Marshall D., 3699
 Slack, James L., 2066
 Slater, Emily P., 3247
 Slaughter, Gayle R., 3960
 Slusher, Leslie B., 2382
 Smale, Stephen T., 5229
 Small, Stephen J., 1654
 Small, W. Curtis, 38
 Smart, Eric J., 5053
 Smith, Alan E., 3886
 Smith, Barbara J., 2647
 Smith, Craig A., 3020
 Smith, Ian C. P., 2752
 Smith, James R., 1372
 Smith, Kendall A., 2794

- Smith, M. Mitchell, 4111, 5301
 Smith, Michael, 329, 3699
 Smith, Russell K., 440
 Smithies, Oliver, 1402, 2769, 4389
 Smit-McBride, Zeljka, 3105
 Söderkvist, Peter, 4314
 Sollner-Webb, Barbara, 458
 Solomon, Frank, 4726
 Solski, P. A., 1523
 Son, Hyeung Jin, 4244
 Sonenberg, Nahum, 2896, 5992
 Song, Jianguo, 4903
 Sorrentino, Vincenzo, 5338
 Soultz, Johann A., 1729
 Southgate, J., 1326
 Souza, David W., 3886
 Spangler, Rudolph, 102
 Spanopoulou, Eugenia, 2216
 Spevak, Walter, 699
 Spieth, John, 1921, 4651
 Sporn, Michael B., 84, 3795, 5222
 Sprague, George F., Jr., 2952
 Sprague, Karen U., 1382
 Sprecher, S. L., 2328
 Srere, Paul A., 38
 Stacey, Dennis W., 2785, 4053
 Stack, Sean P., 240
 Staeheli, Peter, 4717
 Stallard, Barbara J., 1448
 Stanley, Edouard, 3399, 4363
 Stapleton, Ann E., 5767
 Stark, George R., 4189
 Stateva, Lubomira I., 4235
 Stavnezer, Edward, 1167
 Steen, Harald B., 3384
 Stein, Gary S., 544
 Stein, Janet L., 544
 Stein, Roland, 1734, 2881
 Steinberg, Robert A., 705
 Steitz, Joan A., 3432
 Stenman, Göran, 2125
 Sterling, Joan F., 894
 Stern, David B., 4380
 Stern, David F., 987
 Stern, Jacqueline, 2558
 Sternglanz, Rolf, 2253
 Stévenin, James, 1258
 Stevens, Jeff, 906
 Stewart, David A., 1372
 Stewart, Mark J., 1638
 Stokke, Trond, 3384
 Stoll, Regine, 3545
 Stone, Elisa M., 2253
 Stone, James C., 3132, 6158
 Storms, Reginald K., 329
 Storti, Robert V., 1901, 6337
 Stott, David, 5534
 Straka, Michael S., 2049
 Strauss, Joseph, 5746
 Strehlow, Inga, 182
 Strich, Randy, 6306
 Strickland, Sidney, 3139
 Strömstedt, Per-Erik, 3379
 Strub, Katharina, 3949
 Struhl, Kevin, 4918
 Sturgill, Thomas W., 1002
 Suen, Ting-Chung, 354
 Sugamura, Kazuo, 1313
 Sugino, Akio, 2576, 2583
 Sugita, Hideo, 344
 Sultzman, Lisa, 2018
 Sun, Hong, 6328
 Sun, Minghua, 6248
 Sun, Xiao-Hong, 5603
 Sunday, Mary E., 3125
 Sutcliffe, J. Gregor, 3484
 Sutherland, Robert L., 5032
 Sutor, Shari L., 4431
 Sutton, Ann, 2133
 Sutton, Claudia A., 4274
 Suva, Larry J., 2503
 Suzuki, Koichi, 344
 Swanson, Larry W., 1739
 Swanson, Mark J., 2253
 Swanson, Michele S., 3009
 Szostak, Jack W., 322, 3390, 6328
 Tachibana, Akira, 3163
 Tachibana, Kouichi, 920
 Tainsky, Michael A., 3573
 Takai, Yoshimi, 1438, 2873, 2909
 Takaku, Fumimaro, 2125, 5527
 Takano, Toshiya, 920
 Takechi, Hajime, 4036
 Talarico, Daniela, 1138
 Tamaoki, Taiki, 5885, 6041
 Tan, Eng, 5266
 Tanaka, Yuetsu, 1313
 Taniguchi, Tadatsugu, 3052
 Tano, Keizo, 4660
 Tansey, Terese, 1901, 6337
 Tartakoff, A. M., 391, 2362, 3879
 Tatchell, Kelly, 1069, 3369
 Tatò, Franco, 3331
 Taub, Rebecca, 381, 1393
 Tebabi, Patricia, 338
 Tesfaye, Abeba, 440
 Teumer, Jeffrey K., 1167
 Tewari, Dinesh S., 1393
 Theiry, Timothy A., 864
 Therrien, Marc, 3492
 Thiele, Dennis J., 476, 1232
 Thieringer, Rolf, 510
 Thomas, Jeffrey, 1921
 Thomas, Matthew L., 4415
 Thomas, N. S. B., 3925
 Thomas, Sheila M., 4371, 4739
 Thompson, Craig B., 3288
 Thompson, Elizabeth, 3699
 Thorley-Lawson, David A., 1614
 Thukral, Sushil K., 1566
 Thweatt, Ray, 3905
 Tice-Baldwin, Kimberly, 3642
 Tilburn, Joan, 795
 Timberlake, William E., 55
 Ting, Jenny P.-Y., 2406
 Ting, Ling-Pai, 5044
 Ting, Paul, 2778
 Tini, Mark, 1531
 Tipper, Donald J., 2620
 Tishkoff, Daniel X., 2593
 Tjong, Kuo-Koewang, 5885
 Tocci, Michael J., 4074
 Tojo, Arinobu, 5527
 Tourkine, Nikolai, 2826
 Toyoshima, Kumao, 833, 6279
 Tozawa, Hideki, 1313
 Tran, Chi T., 2263
 Traut, Walther, 2229
 Travali, Salvatore, 731
 Travis, Adam, 5756
 Trawick, John, 2049
 Tredup, Jeffrey, 4398
 Trepte, Hans-Heinrich, 2980
 Trézéguet, Véronique, 2744
 Triglia, Tony, 5244
 Trotter, Joseph, 4779
 Trueman, Laurence J., 4235
 Trumbly, Robert J., 3307
 Truss, Mathias, 3247
 Tsai, Fong-Ying, 4966
 Tsai, Men-Hwei, 2785
 Tsai, Ming-Jer, 4998
 Tsai, Sophia Y., 4998
 Tsay, Yim Ha, 620
 Tseng, Janet C., 1538
 Tsiachlis, Philip N., 2864
 Tsui, Lap-Chee, 1531
 Tsukahara, Toshifumi, 344
 Tucker, G., 3879
 Tucker, Philip W., 5197, 5206
 Tukey, Robert H., 4314
 Tung, Lin, 1048
 Turck, Christoph W., 1125
 Turc, Beatrice, 4022
 Tzagoloff, Alexander, 3931
 Tzukerman, Maty, 4097
 Udvardy, Andor, 4973
 Ueyama, Hisao, 3296
 Ullrich, A., 1454
 Ullrich, Axel, 913
 Umezawa, Akihiro, 920
 Ursic, Doris, 2629
 Usman, Nassim, 3390
 Usuda, Sadakazu, 4528
 Vacca, Alessandra, 4771
 Vakalopoulou, Evangelia, 3355
 Valancius, Vicki, 1402, 4389
 Valencik, Maria L., 2399
 van der Geer, Peter, 4698
 Van der Ploeg, Lex H. T., 2467, 3180, 3823
 van der Valk, Martin, 1176
 Vande Woude, George F., 604, 5985
 Van Dyke, Terry, 5968
 van Hoffen, Anneke, 4128
 van Lohuizen, Maarten, 1176
 van Loon, Adolphus P. G. M., 259, 2315
 Van Wart Hood, Jill E., 4282
 van Zee, Karen, 5137
 van Zeeland, Albert A., 4128
 Varanasi, Ushasri, 3307
 Vardimon, Lily, 5275
 Varesio, Luigi, 2718
 Varnum, Brian C., 1754
 Varticovski, Lyuba, 1107
 Vasavada, Haren A., 3564
 Vass, William C., 2819, 6026
 Vassalli, Pierre, 2826
 Vaughan, Martha, 1146
 Vaughn, J. P., 3850
 Veloz, Linda, 4065
 Velu, Thierry J., 6026
 Venema, Jaap, 4128
 Venkov, Pencho V., 4235
 Vera, Juan C., 3407
 Verbeek, Sjef, 1176
 Vidal, Marc, 6306, 6317
 Vigna, Elisa, 1793
 Vignais, Marie-Luce, 2641
 Vilen, Barbara J., 2406
 Villa-Garcia, Manuel, 954
 Villanueva, Mercedes S., 6139
 Vines, Richard R., 945, 5113
 Viskochil, David, 906
 Voelker, Robert A., 894
 Voellmy, Richard, 3660, 5937
 Vogel, Ursula S., 2812
 Vogelstein, Bert, 1724
 Vogt, Volker M., 2282
 Vojtek, Anne, 1248
 Volland, C., 1114
 Voronova, Anna, 1156
 Vos, Jean-Michel H., 2245
 Vuocolo, Gerald A., 2307
 Wad, Paul A., 4555
 Wagner, John, 3504
 Wahl, Geoffrey M., 4779
 Wahl, Walter, 2937
 Walbot, Virginia, 533
 Walker, Lisa, 1372
 Walker, Michael D., 1547
 Walker, P. Roy, 2752
 Walker-Jonah, Annie, 5454
 Wall, Randolph, 1409
 Wallace, Helen, 4207
 Walliker, David, 963
 Walsh, Ken, 3735
 Walsh, Kenneth, 1944, 6296
 Walter, Gernot, 1988, 1996, 4282
 Walter, Peter, 3949
 Wambach, Marlene, 5497
 Wandersee, Nancy J., 4690
 Wang, Bin, 5426
 Wang, C. Kathy, 4809
 Wang, Hwa-Chain R., 945
 Wang, Hwei-Gene Heidi, 4253
 Wang, Janet M., 4545
 Wang, Jean Y. J., 1553
 Wang, Jiyang, 75
 Wang, Lu-Hai, 4165
 Wang, Teresa S.-F., 2081
 Wang, Tongtong, 166
 Wang, Weidong, 4561
 Wang, Yan, 3554
 Wasielenko, William J., 309
 Wasserman, David A., 3432
 Wasyluk, Bohdan, 5381
 Wasyluk, Christine, 5381
 Watanabe, Takeshi, 75
 Watanabe, Yonosuke, 920
 Wauthier, Eliane L., 2245
 Wawrousek, Eric F., 4340
 Weaver, Casey T., 4415
 Weaver, David T., 3155
 Webb, Carol F., 5197, 5206
 Weber, Lee A., 544
 Weber, Michael J., 309, 1002, 2812, 4448
 Webster, Leland C., 4287
 Wegrzyn, Ronald J., 2307
 Weiden, Michael, 3823
 Weidenhammer, Elaine, 5801

- Weil, P. Anthony, 1734, 2881, 4809
 Weinberg, Eric S., 1048
 Weinrich, Scott L., 4985
 Weinstein, I. Bernard, 3915
 Weis, Frances M. B., 4952
 Weiss, Karen E., 1590
 Weisschart, Klaus, 4786
 Weissman, Jocelyn D., 4217, 4228
 Weissman, Sherman M., 3564
 Weith, Andreas, 2229
 Wek, Ronald C., 3027
 Welham, Melanie J., 2901
 Welles, Thomas E., 3326
 Wellinger, Raymond J., 2919
 Welsh, Michael J., 3699, 3886
 Werner, Sabine, 4627
 Wessler, Susan R., 6192
 Wexler, Daniel, 3191
 Whelan, James, 2881
 Whetsell, Lynne, 5902
 Whetsell, Michael, 5902
 White, Charles I., 5372
 White, Gretchen, 1180
 White, Gretchen A., 5985
 White, Kalpana, 2994
 White, Martyn K., 4448
 White, Morris F., 3191
 White, Ray, 906
 White, Terry B., 3369
 Whitesell, Luke, 1360
 Whoriskey, John, 2004
 Wickner, Reed B., 2905
 Widner, William R., 2905
 Widom, Russell L., 677, 3814
 Wigler, Michael, 1248, 3554
 Wilcox, Josiah N., 3454
 Wilhelmsson, Anna, 401, 4314
 Wilks, Andrew F., 2057
 Williams, Bryan R. G., 5497
 Williams, David A., 4518
 Williams, Douglas E., 3043
 Williams, Frederick E., 3307
 Williams, Lewis T., 1125, 4627
 Williams, Paul (Mickey), 4959
 Williams, Steven R., 5860
 Williams, Suzanne P., 6139
 Wills, Ken N., 6016
 Willumsen, Berthe M., 6026
 Wilson, Gloria, 1765
 Wilson, Robert B., 3369, 6185
 Wilson, Sandra J., 3711
 Wilusz, Jeffrey, 5312
 Wingfield, Paul, 2567
 Winking, Heinz, 2229
 Winokur, Thomas S., 5222
 Winqvist, Robert, 4015
 Winsor, Barbara, 3075
 Winston, Fred, 3009, 5710
 Wise, Carol A., 1662
 Withers, Donald A., 4846
 Witte, Owen N., 854, 1785, 1854, 4710
 Wold, Barbara J., 2842
 Wolff, Thorsten, 2026
 Wolffe, Alan P., 655
 Won, Kwang-Ai, 3001
 Wong, G., 1523
 Wong, Min-Liang, 5497
 Wongsasant, Budsaba, 6279
 Wood, Carla M., 1372
 Wood, Rachel M. C., 5330
 Wood, William G., 4679
 Wooden, Scott K., 5612
 Woodgett, James R., 5541
 Woodward, Jerold G., 578
 Wool, Ira G., 3842
 Woolford, John L., Jr., 5681
 Woontner, Michael, 4555
 Wrangle, Örgan, 5259
 Wright, David A., 6248
 Wright, Robin, 5801
 Wright, Woodring E., 4104
 Wu, C.-Ting, 3940
 Wu, Hong, 5113, 5154
 Wu, Kou-Juey, 4423
 Wu, Michael, 1965
 Wu, Min, 166
 Wubbolts, Richard, 5963
 Xu, Gangfeng, 906
 Xu, Hao-Peng, 3554
 Xu, Hua, 2736
 Xu, Lin, 6007
 Xue, Chu-Biao, 1030, 3603
 Yaciuk, Peter, 2116, 5389
 Yaffe, Michael P., 2647
 Yamada, Kenneth M., 4036
 Yamagishi, Masahiro, 746
 Yamagoe, Satorini, 3522
 Yamaguchi, Masamitsu, 4909
 Yamamoto, Masayuki, 2778, 3088
 Yamamoto, Tadashi, 833
 Yamamoto, Takeshi, 2873
 Yamamoto, Tohru, 4809
 Yan, Duen-Hwa, 1875
 Yanagida, Mitsuhiro, 5839, 6093
 Yang, Austin J., 4278
 Yang, Beom-Seok, 2291
 Yang, Sung-Il, 1988
 Yang, Weimin, 3676
 Yano, Ryoji, 754
 Yanofsky, Charles, 928, 935
 Yao, Kwok-Ming, 2994
 Yarden, Y., 1454
 Yasuda, Hisataka, 6041
 Yean, Shyue-Lee, 5571
 Yen, T. S. Benedict, 1353
 Yew, Nelson, 604
 Yi, Taolin, 2391
 Yi, Tau-Mu, 1944
 Yim, Sun O., 3573
 Yoas, Karen, 6067
 Yoshida, Kazuya, 4528
 Yoshimura, Akihiko, 1980
 Yoshioka, Takayuki, 5479
 Yost, H. Joseph, 1062
 You, Yun, 1133
 Young, Elton T., 1566
 Young, Judy C., 854, 1785
 Young, Lisa S., 1382
 Young, Richard A., 4669, 5781
 Youssoufian, Hagop, 1980
 Yu, Chun-Li, 2785
 Yu, Dihua, 1745
 Yu, Jin-Chen, 3780
 Yuan, Gwo-Fang, 5735
 Yuan, Yan, 5266
 Yuan, Yi-Lu O., 5910
 Yuh, Chiou-Hwa, 5044
 Yutzey, Katherine E., 267
 Zakian, Virginia A., 2919
 Zanolari, Bettina, 5251
 Zaret, Kenneth S., 773, 4405
 Zentella, Alejandro, 4952
 Zerillo, Cynthia, 987
 Zhan, Xi, 1840
 Zhang, J. T., 363
 Zhang, Ke, 2819, 3132
 Zhang, Xiao-kun, 6016
 Zhang, Yi, 6109
 Zheng, Pan, 987
 Zhou, Dao-Xiu, 1353
 Zhu, Hong, 175, 2273
 Zhu, Jiguang, 5346
 Ziegler, Steven F., 3052
 Ziemiecki, Andrew, 2057
 Zilberstein, Asher, 913, 4739
 Zillmann, Martin, 5410
 Ziman, Michael, 3537
 Zindy, Frederique, 1171
 Zinkel, Sandra S., 5190
 Zisman, Yaffa, 126
 Zitomer, Richard S., 5639
 Zmuidzinas, Antanina, 2794
 Zoidl, Christiane, 93
 Zollman, Susan, 1538
 Zolnierowicz, Stanislaw, 5767
 Zon, Leonard I., 1980
 Zürcher, Gisela, 2057
 Zvibel, Isabel, 108
 Zwollo, Patty, 6185

SUBJECT INDEX

VOLUME 11

- 3'-5' exonuclease active site
DNA polymerase, α -like
polymerization activity, 4786
- 3'→5' exonuclease activity
B lymphocytes, 4398
- 3T3 cell variant
mitogen-activated protein kinase, defective regulation of, 1002
tetradecanoyl phorbol acetate, mitogenically nonresponsive to, 1002
- 3T3 cells
serum stimulated, 381
- 3T3 fibroblasts
c-myc, constitutive expression of
insulinlike growth factor 1, abrogation of requirement for, 731
- 3T3-F442A fibroblasts
eIF-2 α kinase
cellular factor, regulation by, 3259
- 4E, eukaryotic translation initiation factor phosphorylation
Src-transformed cell lines, 2896
- 5' splice site
natural and cryptic, selection between exon sequence, major determinant, 4581
- 5' splice sites, distal alternative
novel protein factor required for use, 5945
- 5' untranslated region
C. elegans
intron insertion, 1921
trans-spliced gene, 1921
- 5S RNA gene
X. borealis
transcription factor IIIA, displacement by transcribing RNA polymerase, 3978
- 6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase
promoter, liver type
protein-binding sites, 1099
regulatory sequences, 1099
- 7SK ribonucleoprotein
human small RNP, 3432
structural analyses, 3432
- 12-O-Tetradecanoylphorbol-13-acetate gap junction proteins
phosphorylation at, expression, modulation of, 5364
- 12-O-Tetradecanoylphorbol-13-acetate response element
ras, activation by
lovastatin, selective inhibition by, 2307
- 20S RNA, naked, 2905
- 25-Hydroxycholesterol
cholesterol-7- α hydroxylase gene, 2049
- 40S nuclear ribonucleoprotein particles
core proteins A2 and B1
(A2)₂B1 tetramers, 864
- 60S ribosomal subunit
S. cerevisiae temperature-sensitive mutants, perturbation in, 5681
- $\alpha 1$ and $\alpha 1$ repression
S. cerevisiae
AAR1/TUP1 protein, 3773
- α -agglutinin
S. cerevisiae
AGA1, 4196
cell adhesion glycoprotein, 4196
cell surface attachment, 4196
- α -Factor
S. cerevisiae
C-terminal cysteine modifications, 3603
degradation by α -mating-type-specific endopeptidase, 1030
G_i arrest recovery, 1030
- A431 epidermoid cells
human
epidermal growth factor receptor tyrosine kinase activity, inhibition of, 2697
tyrphostin, rapid uptake of, 2697
- A+U-rich element RNA-binding factor
c-myc mRNA stability regulation in vitro, 2460
- A' protein
U2 small nuclear ribonucleoprotein particle assembly
leucine periodicity, 1578
protein-protein interactions, 1578
- A-activator-binding site
promoter module
acute-phase genes, 93
vitellogenin gene, 93
- AAR1/TUP1 protein
S. cerevisiae
 $\alpha 1$ and $\alpha 2$ repression, 3773
cell type control, 3773
G protein β subunit, similar structure, 3773
- AAR2 gene
S. cerevisiae
cell type control, 5693
MATA1 cistron pre-mRNA splicing, 5693
- Abasic site, synthetic
repair
DNA synthesis followed by excision and ligation, 4441
- Abelson murine leukemia virus
pre-B cell transformation, 1590
interleukin-7 retroviruses, 1590
- c-abl* function activation
bcr/abl fusion proteins
microfilament binding, 1553
tyrosine kinase, 1553
- abl* oncogene variants
phosphatidylinositol 3-kinase activation, 1107
- ACE2
S. cerevisiae
metallothionein expression activator, 476
SW15 homology, 476
- Acinar genes
transcriptional activation
exocrine pancreas transcription factor 1, 4985
- ACT1
S. cerevisiae
complementation by chicken β -actin gene, 213
disruption, 213
- Activin-A
fetal-rat parietal bone, 250
osteoblast-enriched cultures, 250
- Acute-phase genes
liver-specific expression, 93
promoter module
A-activator-binding site, 93
vitellogenin gene, 93
- Acyl coenzyme A oxidase
C. tropicalis
isozyme function, 4333
sequential gene disruption, 4333
- ADE6 gene
ADH1 promoter, 289
S. pombe
mitotic and meiotic recombination, stimulation by strong ADH1 promoter, 289
- Adenosine deaminase gene
human
transcriptional arrest in exon 1, sequence requirements for, 6248
- Adenosine deaminase gene exon 1
mouse
premature 3' end formation in a cell-free transcription system, 5398
- Adenovirus
major late transcription unit
temporal poly(A) site switching, sequences regulating, 5977
- Adenovirus E1A
splicing of transcripts containing abnormally short introns in vitro
U small nuclear ribonucleoprotein particle interactions, differential block of, 1258
zinc finger protein GLI
cooperation with for transformation, 1724
- Adenovirus E1A gene products
p3000-associated transforming function
simian virus 40 large-T antigen, complementary biological activity of, 2116
- Adenovirus E4 promoter
E1A-mediated activation
E4F cellular transcription factor, independence of, 4297
- Adenovirus type 5 E1A gene products
neu oncogene transformation suppression, 1745
- Adenylate cyclase
S. cerevisiae
GTPase-activating protein IRA1, interactions with, 4591
- Adenyllyl cyclase complex
S. cerevisiae
bifunctional component CAP, 1248
CAP, 1248
- ADH1 promoter
S. pombe
mitotic and meiotic recombination at ADE6 gene, stimulation of, 289
- ADH2
S. cerevisiae
ADH1, activation by, 1566
- ADH2 poly(A) site
S. cerevisiae
3'-end formation efficiency, 2004
upstream point mutations, 2004

- ADH3 gene**
human
retinoic acid response element, 1638
retinoic acid synthesis regulation, 1638
- Adipocyte differentiation**
colony-stimulating factor 1 expression, 920
- Adipose P2 gene expression**
preadipocytes, human
C/EBP-binding region, 2303
- ADRI**
S. cerevisiae
peroxisomal protein genes, positive regulation of transcription, 699
- ADRI transcription factor**
S. cerevisiae
ADH2 activation, 1566
monomers, two, 1566
palindromic sequence binding, symmetrical, 1566
- AGA1**
S. cerevisiae
a-agglutinin, cell surface attachment of, 4196
- AGP/EBP(LAP)**
rat hepatoma cells
alpha-1 acid glycoprotein gene, glucocorticoid induction of, 4959
multiple promoter sites, interaction with, 4959
- Alcohol dehydrogenase gene**
human
ADH3, 1638
retinoic acid response element, 1638
retinoic acid synthesis regulation, 1638
- Alpha-1 acid glycoprotein gene**
glucocorticoid induction
AGP/EBP(LAP), 4959
- $\alpha 1(I)$ collagen gene**
human
tissue-specific expression, 2066
transgenic mice, 2066
upstream regulatory region, 2066
- $\alpha 1$ -Acid glycoprotein gene**
rat
interleukin-1 response element, interaction with NF- κ B, 3001
- Alpha interferon**
signal transduction pathways, two distinct
guanylate-binding protein gene transcription, 5147
transcriptional induction
guanylate-binding protein gene promoter, overlapping elements in, 182
- α Mating type**
S. cerevisiae
a-factor-degrading endopeptidase, 1030
- α -Actin gene**
skeletal
cis-acting promoter serum response elements, 5090
negative-acting nuclear factor, 5090
nonmyogenic cells, 5090
replicating myoblasts, 5090
serum response factor-binding complexes, 5090
- α -Actin promoter**
avian
E12, 2439
myogenic helix-loop-helix regulatory factors, 2439
myogenic induction of, 2439
- α -Actin promoter, skeletal**
common factor 1 transcriptional activator binding, 1765
- α B-crystallin gene**
mouse
lens and skeletal muscle, expression in, 4340
muscle-preferred enhancer, 4340
- α -Factor**
S. cerevisiae
internalization and response during cell cycle, 5251
- α -Factor prohormone maturation**
S. cerevisiae Vps18p, 5813
- α -Globin gene cluster**
human
major regulatory element, 4679
- α -Ketoglutarate dehydrogenase complex**
S. cerevisiae mitochondria, 3931
- α -Like DNA polymerase**
polymerization activity
3'-5' exonuclease active site, 4786
- α -Mannosidase gene**
D. discoideum
cell density, 3339
developmental regulation, 3339
- Alu domain**
signal recognition particle RNA, 3949
- Amino acid starvation**
asparagine synthetase gene expression, regulation of, 6059
- AMPDI gene**
rat
alternative transcript production, 5356
exon recognition, 5356
nucleocytoplasmic partitioning, 5356
- Amphiregulin**
human keratinocyte autocrine factor, heparin sulfate regulated, 2547
- Androgen responsiveness**
 β -glucuronidase gene, mouse
haplotype-specific sequence diversity within intron 9, 5426
nuclease hypersensitivity within intron 9, 5426
protein binding within intron 9, 5426
- Angiotensinogen gene-inducible enhancer-binding protein 1**
nuclear factor κ B-binding site recognition
large nuclear proteins, new family of, 2887
zinc finger motif, 2887
- Apn1 apurinic endonuclease/3'-diesterase**
S. cerevisiae
DNA damage, control of, 4537
spontaneous mutation, control of, 4537
- Apolipoprotein AI gene**
liver cells
transcription factors, synergistic interactions, 677
retinoic acid-responsive element, 3814
- ARG4 locus**
S. cerevisiae
poly(dA · dT) tract, 322
recombination initiation site, 322
- ARG5,6 promoter**
S. cerevisiae
binding of ARGR proteins, 2162
- Arginine anabolic and catabolic pathways**
S. cerevisiae
ARGRII protein, 2169
- Arginine anabolic and catabolic promoters**
DNA-binding sequences of ARGR proteins, 2852
- ARGR proteins**
DNA-binding sequences
arginine anabolic and catabolic promoters, 2852
S. cerevisiae
ARG5,6 promoter, binding to, 2162
- ARGRII protein**
S. cerevisiae
arginine anabolic and catabolic pathways, regulation of, 2169
- ARS elements**
HML mating-type locus silencers
chromosomal DNA replication origins, 5346
S. cerevisiae, 5346
- Asparagine synthetase gene expression**
amino acid starvation, regulation by, 6059
- Asparagine synthetase genes**
transcription repression by light
photosynthetic and nonphotosynthetic organs, 4966
- Aspergillus nidulans**
creA gene
carbon catabolite repression, regulation of, 5701
nirA, 795
four introns in highly conserved regions, 5746
GAL4-type zinc finger protein, 5746
nitrate assimilation pathway-specific regulatory gene, 5746
nitrate assimilation, 795
wetA
spore-specific gene expression, activation of, 55
spore-specific gene expression, regulation of, 47
- ATBF1**
 α -fetoprotein enhancer-binding protein, human
four homeodomains and seventeen zinc fingers, 6041
"Attenuator domain"
C/EBP, 1480
- AU-rich domains**
3' untranslated regions of rapidly degraded mRNAs
protein binding, 3355
- Autocrine growth factors**
clonal growth of tumors, 108
heparin and hormonal regulation of abundance, 108
- Autocrine mechanism of transformation**
induction
K-fgfhst oncogene, 1138
mitogenic pathway, extracellular stimulation, 1138
- Autonomously replicating sequences**
S. cerevisiae
cell division cycle, 5301
chromatin structure, 5301
- Autophosphorylation**
c-erbB-2 protein carboxyl-terminal domain, 833
MET proto-oncogene tyrosine kinase, activation of, 1793
- Avian α -actin promoter**
E12, 2439
myogenic helix-loop-helix regulatory fac-

- tors, 2439
 myogenic induction of, 2439
axl transforming gene
 primary human myeloid leukemia cells, 5016
 receptor tyrosine kinase, novel, 5016
- B1 factor**
X. laevis
 mammalian activator USF, close relation to, 412
 TFIIIA gene expression, developmental regulation, 412
- B cell**
 E2-box-binding factors
 E12/E47-like subunits, 1156
- B lymphocytes**
 3'→5' exonuclease activity, 4398
 Epstein-Barr virus infection
c-fgr exon, novel, 1500
- B lymphoid cell development**
 immunoglobulin enhancer repression
 by helix-loop-helix protein Id, 6185
- BALB/c-3T3 fibroblasts**
 interferon- β , resistance to growth inhibition by
 aberrant growth factor signal transduction, 3148
- Base-pair mismatch repair**
S. cerevisiae meiotic recombination, 737
- Basic fibroblast growth factor**
 localization
 cytoplasmic, 573
 nuclear, 573
 translation initiation, alternative localization, 573
- B-cell hybridoma**
 interleukin-6
junB transcription, 1409
 TIS11 gene transcription, 1409
- B-cell-specific enhancer element**
 immunoglobulin gene
 regulation, positive and negative, 75
- bcl-1 gene**
 candidate, characterization of, 4846
- BCR**
 first exon sequences
BCR/ABL tyrosine kinase oncogene activation, 1785
 leukemias, human, Philadelphia chromosome positive, 1785
- BCR promoter**
 Philadelphia chromosome-negative cell lines, 1854
 Philadelphia chromosome-positive cell lines, 1854
- bclabl fusion proteins**
c-abl function activation
 microfilament binding, 1553
 tyrosine kinase, 1553
- BCR/ABL oncogene**
 two forms
 oncogenic potency differences, 4710
 target cell specificity, 4710
- BCR/ABL tyrosine kinase oncogene**
BCR first exon sequences, activation by, 1785
 leukemias, human, Philadelphia chromosome positive, 1785
- bcl**
S. cerevisiae
SRK1, suppression by, 3369
- β cells**
 insulin gene expression, 1547
 specific transcription factor IEF1, 1547
- β -Actin gene**
 chicken
 complementation of *S. cerevisiae* *ACT1* gene disruption, 213
- β B1 crystallin gene**
 chicken
 non-lens genes, 1488
 octamer-binding-like promoter elements, 1488
 polyomavirus enhancer-like elements, 1488
- β -Casein gene promoter regulation**
 hormone-mediated relief of transcriptional repression, 3745
 mammary gland-specific nuclear factor, 3745
- β -Glucuronidase gene**
 mouse
 androgen responsiveness, 5426
 haplotype-specific sequence diversity within intron 9, 5426
 nuclease hypersensitivity within intron 9, 5426
 protein binding within intron 9, 5426
- β -Major-globin gene**
 mouse
 erythroid differentiation, derepression of transcription during, 4324
- β -Transducin**
S. cerevisiae homolog
CDC20 gene product, 5592
- β -Tubulin**
 codon change
D. melanogaster, drastic effect on microtubule structure in, 4726
S. cerevisiae, failure to produce significant phenotype in, 4726
- BHK cells**
 chemically transformed phenotype
 suppression by human cDNA, 5321
- Bipartite enhancer element**
 exocrine pancreas transcription factor 1 binding, 4985
- BLAST-1, 1614**
- Bovine papillomavirus**
 E5 oncogene
ras, cooperation with, 6026
- Box- α and box- β**
 hepatitis B virus second enhancer
 C/EBP-like protein binding, 5044
- Brain, developing**
 mouse
myc family gene expression, complex transcriptional regulation of, 6007
- Breast cancer**
 cell cycle inhibition and stimulation
 progestins, 5032
- byr2**
S. pombe
 protein kinase, 3554
ras1 mutant phenotype, partial suppression of, 3554
- bZIP domain**
S. cerevisiae GCN4, 4918
- C6 zinc finger**
 LAC9 transcription activator, 1777
- C/EBP**
 "attenuator domain," 1480
 transactivation domains, 1480
- C/EBP-binding region**
 adipose P2 gene expression
 preadipocytes, human, 2303
- C/EBP-like protein**
 hepatitis B virus box- α and box- β of the second enhancer, binding to, 5044
- Ca²⁺/calmodulin-dependent protein kinase, novel**
 calmodulin-binding protein
 male germ cell specific, 3960
- Cachectin/tumor necrosis factor**
 colony-stimulating factor 1 induction, 920
- Caenorhabditis elegans***
 5' untranslated region
 intron insertion, 1921
trans-spliced gene, 1921
- elt-1**
 embryonic expression, 4651
 GATA transcription factor homology, 4651
- Calcium ionophore**
grp78 promoter transactivation, 5612
- Calmodulin-binding protein**
 male germ cell specific
 novel Ca²⁺/calmodulin-dependent protein kinase, 3960
- Canary**
myc family genes, 1770
- Candida (Torulopsis) glabrata***
 mitochondria
 RNase P activity, 1662
 RNase P RNA, bacterial, 1662
- Candida tropicalis***
 acyl coenzyme A oxidase
 isozyme function, 4333
 sequential gene disruption, 4333
- CAP**
S. cerevisiae
 adenyl cyclase complex, bifunctional component of, 1248
- Carbon catabolite repression, regulation of**
A. nidulans
creA gene, 5701
- Cardiac actin gene promoter**
 human
 CARG boxes, multiple, 4796
 embryonal carcinoma cells, 4796
 embryonic cardiac muscle cells, 4796
- Cardiac muscle cells, embryonic**
 cardiac actin gene promoter, human
 CARG boxes, multiple, 4796
 embryonal carcinoma cells, development in vitro from, 4796
- Cardiac myosin light-chain 2 gene**
 chicken, 1676
 rat myocardial cells
 28-base-pair element, conserved, 2273
 α -adrenergic-inducible expression, 2273
 cardiac-specific expression, 2273
 tissue-specific transcription, 1676
 upstream repressor element, regulation by, 1676
- CARG motif**
 DNA elements, natural and synthetic
 expression and protein-binding properties, differences in, 6296

- Casein kinase II
serum response factor DNA-binding activity
mechanism of increase, 3652
- Catalase A
S. cerevisiae peroxisomes, import into, 510
- CBP1
S. cerevisiae
mitochondrial function, induction of, 813
mRNA 3' end formation, 813
- CCAAT box-binding factor
major histocompatibility complex class II genes promoter, 578
- CCG1 gene
human
G₁ phase progression, 3317
nuclear DNA-binding protein, 210 kilodalton, 3317
- CD4 gene
mouse
T-cell-specific enhancer, 5506
- CD8⁺ T-cell clones
CD45 protein tyrosine phosphatase deficiency
T-cell receptor stimuli, impaired responses to, 4415
- CD44 gene
human
neuroblastoma cells, repression of expression in, 5446
- CD45 protein tyrosine phosphatase
CD8⁺ T-cell clones
T-cell receptor stimuli, impaired responses to, 4415
- CD48, 1614
- Cdc2, inactivation of
S. pombe
Suc1 binding, mutations affecting, 6177
- CDC7
S. cerevisiae
HMR, repression of transcription at, 1080
- CDC20 gene product
S. cerevisiae
 β -transducin homolog, 5592
microtubule-dependent cellular processes, requirement for subset of, 5592
- CDC25
S. cerevisiae
SDC25 similarity, 202
- CDC25 protein
S. cerevisiae
exchange of guanine nucleotides bound to Ras, 2641
- CDC42Sc
S. cerevisiae
GTP-binding protein involved in cell polarity, putative, 3537
mutational analysis, 3537
- CDC55
S. cerevisiae
cellular morphogenesis, 5767
mammalian type 2A protein phosphatase B subunit, homology to, 5767
- CDC68
S. cerevisiae
carboxyl terminus, highly acidic, 5718
proliferation and transcription, regulation of, 5718
- CDEIII sequence
S. cerevisiae centromere
mitotic chromosome separation, requirements for, 5212
- Cell cycle
H3 histone mRNA
changes in stability during, 544
phase-specific modification
E1A-associated 300-kDa product, 5389
nuclear phosphoprotein, stable, 5389
S. cerevisiae
 α -factor internalization and response, 5251
- Cell cycle progression
Fos protein family, requirement for, 4466
Jun protein family, requirement for, 4466
- Cell cycle regulatory unit
thymidine kinase gene, human
cellular factors, interaction with, 2296
- Cell cycle stage-dependent transcription
S. cerevisiae
short, *cis*-acting DNA sequence, 329
- Cell cycle transitions
X. laevis
cyclins B1 and B2, 3860
- Cell death, programmed
thymocytes, immature
mRNAs, 4177
- Cell division cycle
S. cerevisiae
chromatin structure of autonomously replicating sequences, 5301
- Cell separation
S. cerevisiae
protein synthesis requirements, 3691
- Cell surface adhesion molecule Po promoter
Tst-1 binding, 1739
- Cell surface proteins
new family
growth regulation, 2864
rat leukocyte antigen MRC OX-44, 2864
- Cell type control
S. cerevisiae
AAR2 gene, 5693
MATa1 cistron pre-mRNA splicing, 5693
- Cell-cell cohesion
modulation by *D. discoideum* lipids, 468
- Cellular elongation factors
minute virus of mice attenuator
regulation of block to transcription elongation, 3515
- Cellular matrix, detergent insoluble
p60^{src} association
SH2 domain deletions, prevention by, 1207
- Central nervous system
demyelination
transgenic mouse, 5479
- Centromere
S. cerevisiae
chromosome loss rates, 2919
excess, 2919
in vivo genomic footprint, 154
S. pombe chromosome I
mitotic and meiotic functions, DNA regions required for, 2206
- Centromere CDEIII sequence
S. cerevisiae
mitotic chromosome separation, requirements for, 5212
- Centromere DNA element I
S. cerevisiae
helix-loop-helix protein CPF1, binding site for, 3545
- Chicken
 β -actin gene
complementation of *S. cerevisiae* ACT1 gene disruption, 213
 β B1-crystallin gene
non-lens genes, 1488
octamer-binding-like promoter elements, 1488
polyomavirus enhancer-like elements, 1488
cardiac myosin light-chain 2 gene
tissue-specific transcription, 1675
upstream repressor element, regulation by, 1676
myosin light-chain 2 gene, 1676
vitellogenin II promoter
positive and negative control elements, complex set of, 2704
vitellogenin gene-binding protein
leucine zipper transcription factor, 4863
rat DBP, relation to, 4863
vitellogenin II promoter control element, binding to, 4863
- Chicken embryo
fibroblasts
HSP47 heat shock protein, 4036
- Chicken embryo fibroblasts
src
glucose transporter isoforms, differential regulation of, 4448
- Chimeric gene
mouse
mdr1 and *mdr2*, exchange of homologous domains, 595
- Chimeric promoter
in vivo stimulation
nuclear factor I binding sites, 2946
- Chimeric toxin
foreign protein sequence substitution, 1751
Pseudomonas exotoxin, 1751
transforming growth factor α , 1751
- Chinese hamster cell lines
Thy⁻ mutator phenotype
deoxyribonucleotide metabolism, cell cycle-dependent variations in, 20
- Chlamydomonas reinhardtii*
exogenous DNA, introduction by electroporation, 2328
 γ -subunit of chloroplast coupling factor I, mutant lacking, 5053
- Chloroplast coupling factor I
 γ -subunit
C. reinhardtii mutant lacking, 5053
- Chloroplast proteins
spinach chloroplast *petD* mRNA, specific in vitro binding to, 4380
- CHO cell
mutant blocked in dolichol-phosphorylmannose synthesis
tunicamycin, correction by, 391
- Cholera toxin
immediate-early response gene JE induction

- cyclic AMP-independent signaling pathway, 102
- Cholesterol-7- α hydroxylase gene
25-hydroxycholesterol
rat hepatoma cells, 2049
- Chorion promoter-binding factors
silkworm
synergistic interactions, 1954
- Choroid plexus
uniform cell-autonomous tumorigenesis
papovavirus large T antigens, 5968
- Chromatid interactions
recombination, intrachromosomal
direct-repeat analysis, 4839
mouse cells, 4839
- Chromatin
class III gene transcription, 655
nucleosomes transfer from parental to replicated, 6257
S. cerevisiae
autonomously replicating sequences, 5301
structure, transition in
transcription complex disruption, 655
transcriptionally activated
torsional stress, evidence for, 6128
Chromatin assembly, inhibition of
X. laevis oocytes
correlation with mouse mammary tumor virus promoter derepression, 5259
- Chromatin structure
topoisomerase II sites of action, primary determinant of, 4973
- Chromosomal proteins
high-mobility-group-like
DNA-binding sequence, highly conserved, 166
T. thermophila macro- and micronuclei, 166
T. thermophila, 166
- Chromosome I
mouse
homogeneously staining region, inherited, 2229
S. pombe
centromere, 2206
mitotic and meiotic functions, DNA regions required for, 2206
- Chromosome 16
human
G_{on} mRNA, different forms, 1146
splicing of gene transcripts, alternative, 1146
- Chromosome loss rates
S. cerevisiae
centromeres, excess, 2919
telomeres, excess, 2919
- Cisplatin-resistant human cell line
UV radiation, cross-resistance to, 2075
UV-modified DNA, overexpression of cellular factors that recognize, 2075
- Citrate synthase
S. cerevisiae CIT2
intramitochondrial functions, regulation of expression by, 38
nonmitochondrial, 38
- Clathrin heavy chain
S. cerevisiae
deficiency, 3868
mutations at numerous loci, 3868
suppression hypothesis, 3868
viability, 3868
- Cleavage-polyadenylation efficiency
 μ mRNA, 2324
- Clock-controlled genes
N. crassa
transcriptional regulation, 558
- Collagen I gene
Mov13 fibroblasts
DNA methylation, absence of, 47
retrovirus-induced interference, 47
- Collagen α 1(I) promoter
murine
nuclear factor I, interaction with, 4065
Sp1, interaction with, 4065
- Colon carcinoma cell line
LIM 1215
autocrine factors, 4005
proliferative and morphologic responses, 4005
- Colony-stimulating factor 1
H-1/A marrow stromal cells
adipocyte differentiation, down-regulation of expression during, 920
cachectin/tumor necrosis factor, induction by, 920
- Colony-stimulating factor 1 receptor
human
ligand-induced conformational changes, 2489
peptide antisera, 2489
phosphatidylinositol 3-kinase binding site, 2489
tyrosine-706 and -807 phosphorylation site mutants
early response gene transcription, 4698
phosphatidylinositol-3 kinase binding and phosphorylation, 4698
- Colorectal cancer
human
S3 ribosomal protein, overexpression of, 3842
- Common factor 1 transcriptional activator
 α -actin promoter (skeletal) binding, 1765
immunoglobulin heavy-chain enhancer binding, 1765
c-myc promoter binding, 1765
- Complementation group C cells
xeroderma pigmentosum
pyrimidine dimers, selective removal of, 4128
- Complex regulatory DNA element
major histocompatibility complex class I gene, 4217
- Convergent transcription from oppositely oriented promoters
D. melanogaster F elements, 5171
- Core proteins A2 and B1
(A2), B1 tetramers, 864
40S nuclear ribonucleoprotein particles, 864
- cot* oncogene
human
protein kinase, putative, 4088
structure and transforming potential, 4088
- Cotransformation
mouse embryonic stem cells, 2769
- COX1
S. cerevisiae, 2399
- cox2
maize mitochondria
RNA editing intermediates of transcripts, 4278
- COX3
S. cerevisiae, 2399
- CPC1
N. crassa
aligned heptad leucines for dimerization, lack of requirement for, 935
bZIP DNA-binding protein, 935
- cpc-1* gene
N. crassa
differential expression during asexual life cycle, 928
- CPF1
helix-loop-helix protein
binding site, 3545
S. cerevisiae, 3545
- creA* gene
A. nidulans
carbon catabolite repression, regulation of, 5701
- CREB
activity, motifs critical for, 1306
cyclic AMP response, 1306
cyclic AMP-responsive gene induction, 1759
glutamine-rich domain, 1306
v-crk oncogene product
phosphotyrosine-containing proteins
association with, domains sufficient for, 1607
- Cryptic 5' splice site
selection
exon sequence, major determinant, 4581
- CTF/NF-1
estrogen receptor
limiting target factor, stabilized interactions with, 2937
transcriptional activation, synergistic, 2937
grp78 promoter transactivation, mediation of, 5612
- Cx43
differentially phosphorylated forms, 363
tissue-specific distribution, 363
- CYB2 gene
S. cerevisiae
CYP1(HAP1) activator, 3762
cytochrome *b₂*, 3762
transcriptional regulation, 3762
UAS1-B2, 3762
- CYC1 gene
S. cerevisiae
TATA elements, two types, 666
- CYC7 gene expression
nuclear protein
S. cerevisiae ROX3 gene, 5639
- CYC8 protein
S. cerevisiae
glucose repression, 3307
protein complex, 3307
TUP1 protein, 3307
- Cyclic AMP
CREB responsiveness, 1306
- Cyclic AMP signaling
modulation by *D. discoideum* lipids, 468
- Cyclic AMP-dependent protein kinase
catalytic subunit maturation defect, 705
- Cyclic AMP-independent signaling pathway
immediate-early response gene JE induction, 102
cholera toxin, 102

- Cyclic amplification and selection of targets (CASTing)
myogenin consensus binding site, 4104
- Cyclic AMP-mediated signal transduction
pp90^{src} phosphorylation, regulation of, 1861
S6 phosphotransferase activity, regulation of, 1861
- Cyclin B
X. laevis meiotic induction
mos^{Xe} coexpression, acceleration by, 1713
- Cyclin degradation control
eggs, amphibian
phosphatase, okadaic acid sensitive, 1171
- Cyclins B1 and B2
X. laevis
phosphorylation, lack of requirement for cell cycle transitions, 3860
- Cyclophilin
endoplasmic reticulum specific, 3484
- CYP1(HAP1) activator
S. cerevisiae
CYB2 gene transcriptional regulation, 3762
- CYS3 regulatory protein
N. crassa
DNA-binding domain, mutational analysis of, 4356
- Cys-His repeat
gene family, 1754
TIS11 primary response gene, 1754
unusual and highly conserved, 1754
- Cystic fibrosis transmembrane conductance regulator
putative nucleotide-binding domains 1 and 2
mutations, paired variants bearing, 3886
- CYT1 gene
S. cerevisiae
cytochrome c₁, 4934
HAP1 and HAP2/3/4, regulation by, 4934
- cyt-20
N. crassa
second function in addition to protein synthesis, 4022
valyl-tRNA synthetases, cytosolic and mitochondrial, 4022
- Cytochrome b₂
S. cerevisiae
CYB2 gene, 3762
- Cytochrome c
mitochondrial import and accumulation
S. cerevisiae cytochrome c heme lyase, 5487
- Cytochrome c heme lyase
S. cerevisiae
mitochondrial import of cytochrome c, role in, 5487
- Cytochrome c oxidase subunit IV gene
ETS domain binding sites, transcriptional activation through, 5631
- Cytochrome P-450IA1 gene
rat
xenobiotic response elements, DNase I-hypersensitive sites, 4314
- Cytokine genes
activation
functional cytokine mRNAs, generation by retroviral splicing events, 5562
intracisternal A-type particle, 5562
murine myelomonocytic leukemia, 5562
- Cytokinesis
S. cerevisiae
protein synthesis requirements, 3691
- Cytoskeleton-associated substrate
pp60^{src}, 5113
- Cytostatic factor activity
mos gene
transforming efficiency, correlation with, 604
- DAL80 gene
S. cerevisiae
GATA factors, homology of product to, 6205
nitrogen catabolic genes, multiple, regulator of, 6205
nitrogen catabolite repression, sensitivity to, 6205
- DAL81 gene product
nitrogen catabolic genes, requirement for induced expression of, 1161
S. cerevisiae
nitrogen catabolic genes, requirement for induced expression of, 1161
- D-E-A-D family
RNA helicases
S. cerevisiae translation initiation factor 4A, conserved residues, 3463
- Deletion repair
homologous recombination
mammalian in vitro system, 445
- Demyelination
transgenic mouse
central nervous system, 5479
- Deoxyribonucleotide metabolism
cell cycle-dependent variations, 20
Chinese hamster cell lines
cell cycle-dependent variations, 20
Thy⁻ mutator phenotype, 20
- Diacylglycerol
v-Src, increase by
type D phospholipase-mediated hydrolysis of phosphatidylcholine, 4903
- Dictyostelium discoideum
 α -mannosidase gene
cell density, 3339
developmental regulation, 3339
drsA suppressor mutants
discoidin lectin expression, translational control of, 3171
- lipids
cell-cell cohesion modulation, 468
cyclic AMP signaling modulation, 468
- Differentiation
hepatic, 773
- Dihydrofolate reductase
mRNA levels, 3726
myogenic cell line terminal differentiation, 3726
synthesis rates, 3726
- Dioxin receptor
activation to DNA-binding form
receptor affinity determination, 401
- Diphtheria toxin
DT388-anti-TFR(Fv), 2200
human transferrin receptor, 2200
single-chain immunotoxins, 2200
- dis3*⁺ gene
S. pombe
110-kDa essential protein, 5839
mitotic control, 5839
- Discoidin lectin expression
D. discoideum drsA suppressor mutants
translational control, 3171
- DNA binding, differential
thyroid hormone receptor
monomeric, homodimeric, and potentially heteromeric forms, 5005
- DNA damage repair
oxidative and alkylation
S. cerevisiae Apn1 apurinic endonuclease/3' diesterase, 4537
- DNA damage and repair, differential introduction of
mammalian genes
RNA polymerases I and II, transcription by, 2245
- DNA polymerase α
cell cycle-specific expression, 3384
nuclear binding, 3384
- DNA polymerase α gene
human
sequences controlling expression in cycling and serum-stimulated cells, 2081
- DNA polymerase, α -like
polymerization activity
3'-5' exonuclease active site, 4786
- DNA polymerase α -primase
DNA synthesis initiation
replication protein A, 2108
T antigen, 2108
- DNA polymerase, novel
N. intermedia LaBelle mitochondrial plasmid, 1696
- DNA repair
c-myc proto-oncogene locus
plasmacytoma induction, 3095
- DNA repair gene
O⁶-methylguanine-DNA methyltransferase gene
DNA-damaging treatments, induction by, 4660
mammalian cells, induction in, 4660
- DNA replication, autonomous
human cells
DNA size, 2263
DNA source, 2263
- DNA sequence recognition
LAC9 transcription activator
base and backbone contacts, 1777
- DNA strand transfer protein α gene
S. cerevisiae, 2576
- DNA strand transfer protein β
S. cerevisiae
DST2 gene, 2583
- DNA synthesis
DNA polymerase α -primase, initiation by
replication protein A, 2108
T antigen, 2108
retrovirus, avian, 1419
simian virus 40
initiation in vitro, 2350
synthetic abasic site repair, 4441
- DNA synthesis blocker
prohibitin
evolutionary conservation, 1372
fibroblasts, 1372
HeLa cells, 1372

- intracellular protein, 1372
- DNA topoisomerase II
- S. pombe*
- functional 125-kDa core polypeptide, 6093
- DNA-binding activity
- FBR (*gag-fos*) protein
- myristylation, alteration by, 765
- DNA-binding protein
- HMG1 related
- V-(D)-J recombination signal probes, isolation with, 4528
- DNA-binding proteins
- muscle gene elements, interaction with, 1944
- DNA-binding proteins, basic helix-loop-helix
- pancreatic β cell insulin gene transcription, 1734
- DNA-damaging treatments
- DNA repair gene induction, 4660
- mammalian cells, 4660
- O⁶-methylguanine-DNA methyltransferase gene induction, 4660
- DNase I-hypersensitive sites
- mouse E β meiotic recombination hot spot, 1813
- Dolichol-phosphoryl-mannose synthesis-blocked mutants
- CHO cell mutant, correction with tunicamycin, 391
- glycophospholipid anchors, no addition to membrane proteins, 391
- Double-strand break repair
- S. cerevisiae*
- tandemly repeated genes, unique pathway in, 1222
- Double-strand gap repair
- homologous recombination
- mammalian in vitro system, 445
- Double-stranded RNA modification activity, regulation of
- human cells, 3719
- DRA promoter function
- major histocompatibility complex class II
- X and Y elements, requirement for stereospecific alignment of, 2406
- Drosophila melanogaster*
- β -tubulin codon change
- microtubule structure, 4726
- D. virilis*, 2994
- elav* gene
- organizational analysis, 2994
- ELAV protein
- functional analysis, 2994
- F elements
- convergent transcription from oppositely oriented promoters, 5171
- fibroblast growth factor-binding protein, 2319
- fushi tarazu homeodomain
- DNA-binding specificity, 3613
- GEBF-I
- induction, developmental and ecdysone, 523
- glue enhancer-binding factor GEBF-I
- induction, developmental and ecdysone, 523
- glue protein genes
- Sgs-7* and *-8*, 2971
- heat shock protein genes, small
- ecdysterone, differential regulation by, 5937
- hsp70* gene
- RNA polymerase II pause at 5' end, 5285
- multidrug resistance gene homologs, 3940
- P1* gene
- ecdysone, induction by, 2913
- regulatory elements, transformation mapping of, 2913
- proliferating-cell nuclear antigen gene promoter
- zerknüllt protein, repression by, 4909
- proto-oncogene *fps/fes*, gene related to life cycle, expression at different times during, 226
- sex-lethal sex determination gene
- late transcripts, 3584
- related polypeptides, multiple, 3584
- Sgs-3* chromatin structure, 523
- Sgs-7* and *-8* genes
- cis*-acting sequences required for expression, 2971
- superoxide dismutase, bovine
- expression, 632
- oxidative stress resistance, augmentation, 632
- suppressor of hairy wing protein
- hsp70* heat shock gene repression, 1894
- suppressor of sable gene
- RNA-binding proteins, polypeptide with regions similar to, 894
- translation initiation
- AUG initiator codon, reduction by mutations upstream of, 2149
- tropomyosin I gene expression
- muscle-specific intron enhancer, regulation by, 1901
- tropomyosin expression, small differences in
- muscle function, significant effects on, 6337
- Drosophila virilis*
- D. melanogaster*, 2994
- elav* gene
- organizational analysis, 2994
- ELAV protein
- functional analysis, 2994
- drsa* suppressor mutants
- D. discoideum*
- discoidin lectin expression, translational control of, 3171
- Drug resistance, development of
- hexose transporter, mammalian, 3407
- Dsl* element, transposable
- maize
- alternative splicing from exon sequences, 6192
- DST2* gene
- S. cerevisiae*
- DNA strand transfer protein β , 2583
- D-to-J_H rearrangement
- immunoglobulin DJ_H, 2096
- promoter-enhancer approximation, 2096
- E1A
- E4 promoter activation
- E4F cellular transcription factor, independence of, 4297
- jun/AP-1*, positive regulation of, 192
- retinoblastoma protein, phosphorylation of
- independence of direct physical association, 4253
- trans*-dominant mutants
- transcription factor binding, 4287
- zinc finger of *trans*-activating domain, 4287
- E1A-associated 300-kDa product
- nuclear phosphoprotein, stable
- cell cycle phase-specific modification, 5389
- E1A-like activity
- F9 embryonal stem cell
- sequences and factors required, 5534
- e1F-2 α kinase
- 3T3-F442A fibroblasts
- cellular factor, regulation by, 3259
- E2A products
- myogenin, dependence on for DNA binding, 3633
- E2-box-binding factors
- E12/E47-like subunits, 1156
- B cell, 1156
- myocyte, 1156
- E4 promoter, adenovirus
- E1A-mediated activation
- E4F cellular transcription factor, independence of, 4297
- E4F cellular transcription factor
- E1A-mediated activation of adenovirus
- E4 promoter, independence of, 4297
- E12
- heterodimers
- binding to element governing myogenic induction, 2439
- E12/E47-like subunits
- E2-box-binding factors
- B cell, 1156
- myocyte, 1156
- E47/E12 helix-loop-helix proteins
- tal-1* oncoprotein enhancer-binding activity, 3037
- Early gene responses
- transforming growth factor β
- growth-suppressive RB function, cells lacking, 4952
- Early response gene
- NGFI-C
- GCGGGGGCG (GSG) element-binding
- protein family member, 3835
- zinc finger transcriptional activator, 3835
- Early response gene transcription induction
- colony-stimulating factor-1 receptor tyrosine-706 and -807 phosphorylation site mutants, 4698
- E β meiotic recombination hot spot
- mouse
- DNase I-hypersensitive sites, 1813
- transcription factor-binding motifs, 1813
- EBP-80
- intracisternal A-particle
- binding, 117
- long terminal repeat promoter methylation response, 117
- transcription factor, 117
- Ecdysone
- P1* gene, induction by, 2913
- Ecdysterone
- D. melanogaster*
- heat shock protein genes, small, regu-

- lation of, 5937
- Ecdysterone receptor
heat shock genes
developmental regulation of, 3660
sequence-specific transcription factor, 3660
- Ecdysterone regulatory elements
transcriptional activation, 1846
transcriptional repression, 1846
- Eggs, amphibian
cyclin degradation control
phosphatase, okadaic acid sensitive, 1171
- eIF-4E initiation factor mRNA
antisense mRNA expression in HeLa cells
cell division times, lengthened, 5435
eIF-4E, reduced levels of, 5435
p220 component of eIF-4E, reduced levels of, 5435
translation rates, diminished, 5435
- eIF-4F and eIF-4B eukaryotic initiation factors
helicase complex intermediates, assembly of, 5992
RNA unwinding in translation, 5992
- Electroporation
C. reinhardtii, 2328
exogenous DNA, introduction into
C. reinhardtii of, 2328
- Elk
brain-specific receptor tyrosine kinase, 2496
tyrosine kinase, brain-specific receptor, 2496
- Elongation complexes
RNA polymerase II
15- or 35-base transcripts, structures when paused after, 1508
- elt-1*
C. elegans
embryonic expression, 4651
GATA transcription factor homology, 4651
- Embryo cells
rat
cotransformation, 6286
c-Jun proto-oncoprotein transactivating function, 6286
- Embryonal carcinoma cells
mouse
LINE-1 RNA, 4804
ribonucleoprotein particles, 4804
- Embryonal stem cell
F9
E1a-like activity, sequences and factors required for, 5534
- Embryonic globin gene expression
erythroid cells, adult
5' flanking sequences, 4690
butyrate stimulation, 4690
- Embryonic neural retina
v-src expression
cell adhesion, alteration of, 5275
glutamine synthetase, prevention of induction of, 5275
histogenesis, inhibition of, 5275
- Embryonic stem cells
gene targeting
length of homology required, 5586
mouse
cotransformation, 2769
gene targeting, 2769
- vectors, insertion and replacement
integration pattern, 4509
target frequency, 4509
- $\text{E}\mu\text{-myc}$ transgene
mouse
 $\text{E}\mu\text{-pim-1}$ transgene, 1176
pre-B-cell leukemia, prenatal, 1176
- $\text{E}\mu\text{-pim-1}$ transgene
mouse
 $\text{E}\mu\text{-myc}$ transgene, 1176
pre-B-cell leukemia, prenatal, 1176
- Encephalomyocarditis virus
ribosome entry site, internal
recombinant provirus, efficient coexpression of two genes from, 5848
- Endoplasmic reticulum
cyclophilin, specific, 3484
vesicle budding, membrane glycoprotein required for, 5727
S. cerevisiae, 5727
- Endoplasmic reticulum protein genes
GRP78, *GRP94*, and *Erp72*
cell growth, 3446
competitive inhibition, 3446
- Endoplasmic reticulum-to-Golgi transport
S. cerevisiae *SLY* gene products, 2980
- Enhancer/silencer domain interaction with
GATA site
platelet factor 4 gene, rat, 6116
- Epidermal growth factor
epidermal growth factor receptor
association with Raf-1, 913
gastrin promoter, transcription from, 2686
human
aromaticity at position 37 not obligatory for activity, 2425
- Raf-1
association with epidermal growth factor receptor, stimulation of, 913
kinase activity, stimulation of, 913
rhoB gene induction, 3682
- Epidermal growth factor receptor
activation, 309
function, suppression of
heterodimerization, 1454
mutation, dominant negative, 1454
gp185^{erbB-2}, 3191
GTPase-activating protein phosphorylation, 2511
juxtamembrane regions, 3191
phosphorylation, 309
progestins, increase in expression by, 5032
- Raf-1 association
epidermal growth factor, stimulation by, 913
signal transduction, specificity of, 3191
src oncogene-transformed cells, 309
tyrosine kinase activity, inhibition of, 2697
- Epidermal growth factor receptor stimulation
pp60^{src} substrate, 120 kilodalton
tyrosine phosphorylation, 713
- Epithelial cell line
transforming growth factor β
T11 gene regulation, 5338
- Epstein-Barr virus
B lymphocytes, infected
c-fgr exon, novel, 1500
human leukocyte adhesion and activation antigen BLAST-1 (CD48) gene, induction of, 1614
- oriP* family of tandem repeats
EBNA-1, role in arresting replication forks, 6268
- Thyroid hormone receptor gene *c-erbA α*
X. laevis early embryonic development
thyroid gland maturation, expression in advance of, 5079, 5079
- erbB-2*
mitogenic signaling pathway
GTPase-activating protein, 2040
phospholipase C- γ , 2040
- c-erbB-2* protein
transforming potential regulation
autophosphorylation at carboxyl-terminal domain, 833
- c-erbB-2/HER2* gene product
phosphorylation
human mammary carcinoma cells, 979
monoclonal antibody, 979
serum growth factor(s), 979
- v-erbB*
extracellular and transmembrane domains
v-src amino-terminal 14 amino acids, functional replacement by, 4760
- ERG8*
phosphomevalonate kinase gene, 620
S. cerevisiae, 620
- Erythroid cells, adult
embryonic globin gene expression
5' flanking sequences, 4690
butyrate stimulation, 4690
- Erythroid differentiation
mouse
 β -major-globin gene derepression, 4324
- Erythroleukemia cell line
human
globin gene expression, negative regulation of, 3528
megakaryocytic differentiation, 3528
mouse
erythropoietin receptor gene, unregulated expression of, 5527
- Erythropoietin receptor
cytoplasmic region
growth-regulatory domains, nonoverlapping positive and negative, 1980
tyrosine phosphorylation, induction of mitogenesis, correlation with, 4895
- Erythropoietin receptor gene
unregulated expression
murine erythroleukemia cell line, 5527
spleen focus-forming virus long terminal repeat, insertion of, 5527
- Escherichia coli*
S. cerevisiae tRNA, 2744
tyrosine tRNA, 2744
- Estrogen receptor
CTF/NF-1
limiting target factor, stabilized interactions with, 2937
transcriptional activation, synergistic, 2937
- Ethanol
nicotine
coinduction of mammalian stress proteins HSP70 and HSP28, 6034
- ETS domain binding sites
cytochrome c oxidase subunit IV gene
transcriptional activation, 5631

- Eukaryotic initiation factors
 eIF-4F and eIF-4B
 helicase complex intermediates, assembly of, 5992
 RNA unwinding in translation, 5992
- Eukaryotic translation initiation factor 4E phosphorylation
 Src-transformed cell lines, 2896
- Euplotes crassus*
 Tec2
 developmentally programmed excision, 4751
 transposon-like element, 4751
- Evi-1*
 zinc finger proto-oncogene, murine
 DNA-binding protein, sequence specific, 2665
- Evi-1* myeloid transforming gene
 retroviral insertions
 transcription activation, 1820
- Evolutionary conservation
 prohibitin
 DNA synthesis blocker, 1372
- Exocrine pancreas transcription factor 1
 acinar genes, transcriptional activation of, 4985
 bipartite enhancer element, binding to, 4985
- Expression site-associated gene
T. equiperdum
 related gene family, 2180
- Extracellular matrix
 hepatocyte morphology, 4405
Int-2/Fgf-3 oncogene product, association with
 cell transformation, 5929
 liver transcription factor modulation, 4405
- Extracellular matrix protein
 transforming growth factor- β 1, control by, 972
- Extracellular signals
 liver transcription factors, regulation of, 773
- Extrachromosomally amplified genes
 replication timing control, 4779
- F9 embryonal carcinoma stem cell
 E1a-like activity
 sequences and factors required, 5534
 transcription factors, multicomponent differentiation regulated, 1686
- F elements
D. melanogaster
 convergent transcription from oppositely oriented promoters, 5171
- FBR (*gag-fos*) protein
 DNA-binding activity
 myristylation, alteration by, 765
- FER tyrosine kinase
 localization, nuclear and cytoplasmic, 1180
- α -Fetoprotein enhancer-binding protein
 ATBF1
 human
 four homeodomains and seventeen zinc fingers, 6041
- α -Fetoprotein expression
 hepatoma, human
 position-dependent silencer, repression by, 5885
- K-fgf/hst* oncogene
 transformation induction
 autocrine mechanism, 1138
 mitogenic pathway, extracellular stimulation, 1138
- c-fgr*
 human
 monocyte-specific enzyme induction in NIH 3T3 cells, 6279
- c-fgr* exon, novel
 Epstein-Barr virus-infected B lymphocytes, 1500
- Fibroblast growth factor-5
 human
 biosynthesis, 1840
- Fibroblast growth factor genes
 human
 common structural arrangement, 4627
 third immunoglobulin domain, receptor forms that differ in, 4627
- Fibroblast growth factor receptor
 tyrosine-phosphorylated carboxy-terminal peptide
 phospholipase C- γ 1 SH2 domain binding site, 5068
- X. laevis*
 developmental expression, 2481
- Fibroblast growth factor-binding protein
D. melanogaster, 2319
- Fibroblasts
 chicken embryo
 HSP47 heat shock protein, 4036
 FosB and short form, FosB/SF transcriptional activators, action as, 5470
 human
 excision repair proficient, 1927
 repair-deficient cells, 1927
 strand bias, cell cycle dependent, 1927
 UV-induced mutations, 1927
 insulin gene expression, 1547
- mouse
 G₀-to-G₁ transition, 2451
 Hox-2.4 homeobox gene activation, oncogenic potential, 554
 Jun and Fos protein expression, 2451
- Fibroblasts, mitogenic activation of
 protein kinases, homologous, activation of, 2517
 tyrosine phosphorylation, 2517
- Fibroblasts, serum stimulated
 serum response factor
 phosphorylation, extensive modification by, 4545
- FK-506
 antifungal properties, 4616
 FKBI, 4616
 immunosuppressant, 4616
 mitogen-induced activation, inhibition of interleukin-2 promoter, 4074
 NF-AT1, 4074
 NFIL-2A, 4074
S. cerevisiae gene, responsive, 4616
- FK506-binding protein
 human
S. cerevisiae peptidyl-prolyl *cis-trans* isomerase, relation to, 1718
- FKBI
S. cerevisiae
 FK-506-responsive gene, distinct, 4616
- FLP recombinase
 half-FRT sites, 4497
 strand exchange, 4497
- strand scission, 4497
 synapsis, 4497
- Fos
 protein family
 cell cycle progression, requirement for, 4466
 Jun, 4466
 thyroid hormone receptor, interaction with
 novel pathway for action, 6016
 transcriptional regulation in vitro
 Jun, 3624
 multiple activator and regulatory domains, interaction among, 3624
- c-fos*
 human
 promoter elements, multiple basal, 1270
 transcription level, 1270
- mouse
 transcription arrest, premature, sequence requirements for, 2832
 progesterins, increase in expression by, 5032
 serum response element
 multiprotein complex, interaction with, 2752
- c-fos* gene transcription
 macrophages, murine
 calcium-dependent block to elongation, 2826
- c-fos* mRNA
 macrophage
 interferon- γ , downregulation by at posttranscriptional level, 2718
- c-fos* promoter
 oncogene-responsive sequences
 cell-specific regulation, 5381
- fosB* gene
 FosB and short form, FosB/SF fibroblasts, transcriptional activation in, 5470
- v-Fps
rhoB gene induction, 3682
- fps/fes*
 related gene
D. melanogaster, 226
 life cycle, expression at different times during, 226
- FUS1* gene
S. cerevisiae
 pheromone response elements, 2952
 transcription, basal and pheromone induced, 2952
- fushi tarazu homeodomain
D. melanogaster
 DNA-binding specificity, 3613
- G₀-to-G₁ transition
 mouse fibroblast cells
 NF- κ B DNA-binding activity, induction of, 4943
- mouse fibroblasts
 Jun and Fos protein expression, 2451
- G₁ arrest
S. cerevisiae
 α -factor degradation, 1030
- G₁ phase progression
 CCG1 gene, human, 3317
- G₁/S-phase growth arrest
 transforming growth factor β 1
 histone H1 kinase activity inhibition,

- 1185
p34^{cdc2} phosphorylation, inhibition of, 1185
- G protein
β subunit
AARI/TUPI protein, similar structure, 3773
- G · C → T · A transversions
S. cerevisiae rad18 mutator, 218
- gadd45* gene
human
ionizing radiation, induction by, 1009
protein kinase C, lack of mediation by, 1009
- gag* gene
Rous sarcoma virus
nonsense codons, 2760
unspliced viral RNA, decreased stability of, 2760
- gag-fos* (FBR) protein
DNA-binding activity
myristylation, alteration by, 765
- GAL1*, galactokinase encoded by bifunctional protein
K. lactis GAL1 gene induction, 5454
S. cerevisiae gal3 phenotype suppression, 5454
- GAL4*
S. cerevisiae
GAL11 (SPT13), phosphorylation by, 2311
- GAL4*-type zinc finger protein
A. nidulans nira, 5746
- GAL11* (SPT13) transcriptional regulator
S. cerevisiae
GAL4 phosphorylation, 2311
- Galactokinase encoded by *GAL1* bifunctional protein
K. lactis GAL1 gene induction, 5454
S. cerevisiae gal3 phenotype suppression, 5454
- Gamma interferon
transcriptional induction
guanylate-binding protein gene promoter, overlapping elements in, 182
- γ-Actin gene
human
chromosome location, 3296
evolution, 3296
expression, 3296
smooth muscle (enteric type), 3296
structure, 3296
- γF-crystallin promoter
mouse
lens cell transcription factor, interaction with, 1531
proximal domain, 1531
- Gap junction proteins
phosphorylation and expression
12-*O*-tetradecanoylphorbol-13-acetate, modulation by, 5364
ras oncogene, modulation by, 5364
- GAS1* protein
S. cerevisiae
glycophospholipid membrane-anchoring determinants, 27
- Gastrin promoter, transcription from epidermal growth factor responsiveness, 2686
- GATA-I site, conserved
human ε-globin gene promoter
transcriptional role of, 2558
- GATA factors
S. cerevisiae DAL80 gene product, homology to, 6205
- GATA transcription factor
C. elegans elt-1 homology, 4651
- GCD2
S. cerevisiae
GCN4 gene, translational repressor of, 3203
protein synthesis initiation, 3203
- GCGGGGGCG (GSG) element-binding protein family
NGFI-C early response gene, 3835
- GCN2 protein kinase
S. cerevisiae
GCN4 gene translational activation, 3027
ribosome association, 3027
- GCN4*
S. cerevisiae
amino acid-starved cells, 486
bZIP domain, highly conserved residues in, 4918
DNA binding, 4918
GCD2, translational repression by, 3203
GCN2 protein kinase, translational activation by, 3027
ribosomal reinitiation at upstream open reading frames, suppression of, 486
translational control, 486
translational regulators, complex formation by, 3217
- GDH2* complex upstream region
S. cerevisiae
NAD-linked glutamate dehydrogenase, role in nitrogen regulation of, 6229
- GDP dissociation stimulator
smg p21 proteins, 2873
- GDP/GTP exchange protein
smg p25A
C-terminal region, 1438
- GDP/GTP exchange protein for *smg* p25A mammalian inhibitory
S. cerevisiae SEC4 protein, action on, 2909
- GBF-I
D. melanogaster
induction, developmental and ecdysone, 523
- Gene rearrangements
mammalian cells
plasmid-based system for study, 3915
- Gene targeting
embryonic stem cells
length of homology required, 5586
mammalian
double-strand gap repair, 4389
mouse embryonic stem cells, 2769
- Germ cells, testis
rat
transferrinlike (hemiferrin) mRNA, 1448
- Germ line ε transcripts
promoter
lipopolysaccharide-plus-interleukin-4 responsive element, 5551
- Germ line-specific splicing
cis-acting sequence, 1538
P element ORF2-ORF3 intron, 1538
- Giardia lamblia*
rDNA genes
telomeric location, 3326
- GLN3*
S. cerevisiae
nitrogen regulatory gene, positive, 6216
putative zinc finger DNA-binding domain on protein, 6216
- Globin gene, embryonic
erythroid cells, adult
5' flanking sequences, 4690
butyrate, stimulation of expression by, 4690
- Globin gene expression
human erythroleukemic cell line
megakaryocytic differentiation, 3528
negative regulation, 3528
- ε-Globin gene promoter
human
GATA-1 site, conserved, transcriptional role of, 2558
- α-Globin genes
human
developmental regulation, autonomous, 3786
transgenic mice, 3786
- α- and β-globin genes
human
transient heterokaryons, 1239
- Globin promoter
nonerythroid cells
trans-activation, 843
- Glucocorticoid
transforming growth factor β1, regulation of, 4490
- Glucocorticoid receptor
binding to sequence overlapping TATA box, 3379
decreased activity, 1647
glucocorticoid receptor antisense RNA gene fragment transfection, 1647
negative regulation, potential mechanism for, 3379
- Glucose repression
S. cerevisiae
GRR1, requirement for, 5101
- Glucose transporter isoforms
chicken embryo fibroblasts
src, differential regulation by, 4448
- Glue enhancer-binding factor GBF-I
D. melanogaster
induction, developmental and ecdysone, 523
- Glue protein genes
D. melanogaster
cis-acting sequences required for expression, 2971
Sgs-7 and -8, 2971
- Glutamate dehydrogenase, NAD dependent
S. cerevisiae
carbon regulation, 4455
- Glutamate dehydrogenase, NAD-linked
S. cerevisiae
GDH2 gene complex upstream region
role in nitrogen regulation, 6229
- Glutamine synthetase gene
position-specific transcription
hepatocyte interaction with collecting (hepatic) veins, 6050
mouse liver, 6050

- Glutathione *S*-transferases
S. cerevisiae URE2 gene product homology, 822
- Glycolipid-anchored membrane proteins
mouse fibroblasts, 2362
- Glycolytic mRNAs
S. cerevisiae
differential regulation, 5330
- Glycophospholipid membrane anchoring
S. cerevisiae GAS1 protein, 27
- Glycosylation block
grp78 promoter transactivation, 5612
- G₂ mRNA
chromosome 16, human, 1146
splicing of gene transcripts, alternative, 1146
- Golgi functions, late
S. cerevisiae Vps18p, 5813
- gp34 glycoprotein
human T-cell leukemia virus type I transactivator p40^{int}, induction by, 1313
- gp185^{erbB-2}
epidermal growth factor receptor, 3191
juxtamembrane regions, 3191
signal transduction, specificity of, 3191
- Granulocyte-macrophage colony-stimulating factor gene promoter
mouse
lymphokine gene element, nuclear factors that interact with, 5894
nuclear factors, lymphokine gene element interaction with, 5894
- Growth factor-mediated signal transduction
pp90^{rsk} phosphorylation, regulation of, 1861
- S6 phosphotransferase activity, regulation of, 1861
- Growth regulation, new family of cell surface proteins involved in, 2864
- Growth-regulatory domains
nonoverlapping positive and negative erythropoietin receptor cytoplasmic region, 1980
- Growth-suppressive RB function
cells lacking
early gene responses to transforming growth factor β , 4952
- GRP78, GRP94, and ERp72
endoplasmic reticulum protein genes
cell growth, 3446
competitive inhibition, 3446
- grp78 promoter
transactivation
calcium ionophore, 5612
glycosylation block, 5612
malformed proteins, 5612
mediation through proximal region containing CCAAT motif which interacts with CTF/NF-1, 5612
- GRR1
S. cerevisiae
glucose repression, requirement for, 5101
leucine-rich repeats, protein with, 5101
- G_s α
Mg²⁺-binding site, putative
activation by receptors, 4830
mutation, 4830
- GTPase-activating protein
C terminus
suppression of *src* transformation, 2819
- epidermal growth factor
phosphorylation by at Tyr-460, 2511
- epidermal growth factor stimulation, 945
- erbB-2 mitogenic signaling pathway
erbB-2 mitogenic potency, 2040
tyrosine phosphorylation, 2040
- inhibition of *v-src*-induced transformation, 2812
- mouse Ras
phospholipids, mitogenically active, association with, 2785
- p21^{ras}
protein-tyrosine kinases, regulation by, 1804
- pp60^{src}
tyrosine-phosphorylated cellular proteins, induction of association with, 945
- ras* effector domain mutant interactions, 3132
- SH2 domains
phosphorylation adjacent to, 2511
- Src kinases, viral and cellular interactions with, 5059
- suppression of *src* transformation, 2819
- GTPase-activating protein homolog
S. pombe, 3088
- GTPase-activating protein IRA1
S. cerevisiae
adenylate cyclase, interactions with, 4591
- GTP-binding protein gene
mouse, transgenic, 886
- GTP-binding protein, putative
cell polarity control
S. cerevisiae CDC42Sc, 3537
- GTP-binding Ypt1 protein
SLY gene products
suppression of defects, 2980
- Guanine nucleotides
IMP dehydrogenase gene, regulation of expression by, 5417
- Guanylate-binding protein gene
transcription activation
alpha interferon-dependent signal transduction pathways, 5147
- Guanylate-binding protein gene promoter
overlapping elements
alpha and gamma interferon, transcriptional induction by, 182
- Guanylate-binding proteins
interferon induced
GMP binding, 4717
N(T)KXD consensus motif, lack of, 4717
- Guide RNA
T. equiperdum minicircles, 1668
- H1
transcriptionally active genes, association with
developmental changes, 1729
- H1/A marrow stromal cells
colony-stimulating factor 1 expression
adipocyte differentiation, down-regulation during, 920
- cachectin/tumor necrosis factor, induction by, 920
- H2B histone gene promoter
X. laevis oocytes
variant octamer motif not required for transcription in oocytes, 641
- H3 and H4 histones
cell cycle progression, normal requirement for, 4111
- N-terminal domains, highly conserved, 4111
- H3 histone mRNA
human
cell cycle, changes in stability during, 544
- H-35 cells
insulin stimulated
immediate-early growth response, 381
- Half-FRT sites
FLP recombinase
strand exchange, 4497
strand scission, 4497
synapsis, 4497
- Hammerhead structures, extended
satellite 2 transcripts, newt
self-cleavage, 6109
- HAP2
S. cerevisiae, 611
S. cerevisiae homolog, 611
S. pombe, 611
small essential core protein domain conservation, 611, 611
- hck
mouse
subcellular localization, 4363
two isoforms, 4363
- Heart
PKC-L, specific expression, 126
- Heart development
rat
neural cell adhesion molecule, 27
alternatively spliced forms, 1654
- Heat shock
S. cerevisiae
proteins, 1062
response, 1062
RNA processing during, 1062
- Heat shock factor
activation, multistep
Ca²⁺, 3365
permeabilized cells, 3365
- mammalian
regulation, resemblance to *S. pombe* and *S. cerevisiae*, 281
- S. cerevisiae*
regulation, resemblance to mammalian and *S. pombe*, 281
- S. pombe*
regulation, resemblance to mammalian and *S. cerevisiae*, 281
- Heat shock factor gene mutation
S. cerevisiae
cell cycle, temperature sensitive defect, 2647
- mitochondrial import, temperature sensitive defect, 2647
- Heat shock genes
developmental regulation
ecdysterone receptor, 3660
- Heat shock protein
HSP47
chicken embryo fibroblasts, 4036
collagen binding, 4036
tissue specific, 4036
transformation sensitive, 4036

- Heat shock protein genes, small
D. melanogaster
 ecdysterone, differential regulation by, 5937
- Heat shock proteins
 hsp90, hsp56, and hsp70
 progesterone enhancement of target gene transcription, 4998
 progesterone receptor free of hsp, 4998
- Heat shock, severe
H. capsulatum
 hsp82 gene, proper splicing of, 5624
- heat shock transcription factor
 human
 hsp70 promoter, 586
 modular recognition of 5-base-pair DNA, sequence motifs, 3504
S. cerevisiae
 metallothionein gene activation, 1232
 metallothionein gene expression, 3676
- Heavy-strand promoter region
 mitochondrial DNA, human, 1631
- HeLa cells
 eIF-4E initiation factor mRNA
 antisense mRNA expression, effects of, 5435
 nuclear extract
 heat inactivated, 3425
 spliceosome assembly, rescue of, 3425
- HeLa nuclear extract
 RNA polymerase II transcription
c-myc, premature termination in, 4599
- Helicase complex intermediates
 assembly
 eIF-4F and eIF-4B, 5992
 RNA unwinding in translation, 5992
- Helix-loop-helix muscle regulatory factors
 transcription factors, ubiquitous, interaction with, 267
 troponin I gene expression, 267
- Helix-loop-helix protein CPF1
 binding site
S. cerevisiae centromere DNA element I, 3545
- Helix-loop-helix protein Id
 immunoglobulin enhancer, repression of B-lymphoid-cell development, implications for, 6185
- Helix-loop-helix proteins
 DNA binding, inhibition of
 Id1 and Id2 proteins, 5603
- Helix-loop-helix transcription factor repressor
 Id, 1040
 immunoglobulin kappa 3' enhancer regulation, 1040
- Hematopoietic cells
lyn kinase, two forms of, 2391
- Hemopoietic growth factors
c-kit mRNA and protein, modulation of, 2901
- Heparin
 autocrine growth factor regulation, 108
 clonal growth of tumors, 108
 mRNA synthesis regulation, 108
- Heparin sulfate
 keratinocyte autocrine factor regulation, 2547
- Hepatitis B virus
 box- α and box- β of the second enhancer
 C/EBP-like protein binding, 5044
- Hepatitis B virus promoter
 transcription activation
 HNF-1 liver-specific factor, 1353
 Oct-1 transcription factor, 1353
- Hepatocyte growth factor receptor
 Met
 C-terminal truncated forms, 5954
MET proto-oncogene, 6084
 tyrosine kinase
 defective posttranslational processing, activation by, 6084
- Hepatocyte morphology
 extracellular matrix, 4405
- Hepatoma
 human
 α -fetoprotein expression, repression by, 5885
 position-dependent silencer, 5885
- Hepatoma cells
 rat
 25-hydroxycholesterol, complementation group with resistance to, 2049
 cholesterol-7- α -hydroxylase gene, 2049
- Herpes simplex virus type 1
 thymidine kinase
 cryptic promoter, 4207
 transgenic mice testes, expression in, 4207
- Heterodimerization
 epidermal growth factor receptor
 mutation, dominant negative, 1454
- Heteroduplex formation
S. cerevisiae
 "stuck" mutation, 5372
- Heterogeneously initiated transcription
mb-1 promoter, pre-B- and B-cell-specific
 initiation site sequences, requirement for, 5756
 upstream factor-binding sites, requirement for, 5756
- Heterokaryons, transient
 human α - and β -globin gene expression, 1239
- Hexose transporter
 mammalian
 drug resistance, development of, 3407
S. cerevisiae HXT1 gene product, 3804
- HIS4
S. cerevisiae
 BAS1/BAS2- and GCN4-dependent transcription, 3642
 RAPI requirement, 3642
- Histone
 3'-processing site
 histone H2a gene, 497
 H3 and H4
 cell cycle progression, normal, 4111
 N-terminal domains, highly conserved, 4111
 H3 mRNA
 cell cycle, changes in stability during, 544
- Histone gene
 human
 transcription factor binding, 5825
- Histone genes
 mouse
 transcriptional activator, common, 2929
- Histone H1
 transcriptionally active genes, association with
 developmental changes, 1729
- Histone H1 kinase activity
 transforming growth factor β 1, inhibition by
 G₁/S-phase growth arrest, 1185
- Histone H2a gene
 mouse
 histone 3'-processing site, intact, 497
 transcription termination, 497
- Histone H2B mRNAs
L. enriettii
 structure and regulation, 240
- Histone H4 gene transcription factor
S. purpuratus
 promoter-binding sites, 1048
 UHF-1, 1048
- Histone mRNA
 regulation in unperturbed cell cycle
 two posttranscriptional steps, control at, 2416
- Histoplasma capsulatum*
 hsp82 gene
 proper splicing in severe heat shock conditions, 5624
- HL60 cells
 NF- κ B
 cyclic AMP-independent activation, 2315
 tumor necrosis factors α and β , 2315
- HMG1
 DNA-binding protein, related
 V-(D)-J recombination signal probes, isolation with, 4528
- HMG chromosomal proteins
 transcriptional activation potential, 4483
- HML mating-type locus
S. cerevisiae
 ARS elements, 5346
 silencers, 5346
- HMR
S. cerevisiae
 CDC7, role in repression of transcription, 1080
 silent mating-type locus, 1080
- HNF-1 liver-specific factor
 hepatitis B virus promoter
 transcription activation, 1353
 Oct-1 transcription factor, 1353
- HO
S. cerevisiae
 SIN1 (SPT2) negative regulator of transcription, 4135
- Homeobox gene
 mouse
 activation, 554
 Hox-2.4, 554
 oncogenic potential, 554
 PBX2 and PBX3
 human proto-oncogene *PBX1*, extensive homology to, 6149
- Homogeneously staining region, inherited
 chromosome 1
 mouse, 2229
- Homologous recombination
 deletion repair, 445
 double-strand gap repair, 445
 mammalian in vitro system, 445
X. laevis oocytes
 nonconservative mechanism, 3278

- single-stranded tails, 3268
- Hormone-mediated relief of transcriptional repression
- β -casein gene promoter activity regulation, 3745
- Hormones
- autocrine growth factor regulation, 108
- clonal growth of tumors, 108
- mRNA synthesis regulation, 108
- Hox1.3 gene
- targeted gene disruption
- promoterless vectors, 5578
- Hox-2.4 homeobox gene
- mouse
- activation, 554
- fibroblasts, 554
- oncogenic potential, 554
- H-Ras:Rap1A chimeric protein
- transformation by
- Rap1A (Krev-1) protein, COOH-terminal domain, 1523
- HSP47
- heat shock protein
- chicken embryo fibroblasts, 4036
- collagen binding, 4036
- tissue specific, 4036
- transformation sensitive, 4036
- hsp70
- D. melanogaster*
- RNA polymerase II pause at 5' end, 5285
- D. melanogaster* suppressor of hairy wing protein, repression by, 1894
- T. brucei*
- polycistronic pre-mRNA maturation, 3180
- HSP70 and HSP28
- stress proteins, mammalian
- nicotine and either ethanol or heat, coinduction by, 6034
- hsp70 promoter
- human
- heat shock transcription factor interaction, 586
- hsp82 gene
- H. capsulatum*
- proper splicing in severe heat shock conditions, 5624
- Human
- A431 epidermoid cells
- epidermal growth factor receptor tyrosine kinase activity, inhibition of, 2697
- tyrphostin, rapid uptake of, 2697
- adenosine deaminase gene
- transcriptional arrest in exon 1, sequence requirements for, 6248
- ADH3 gene
- retinoic acid response element, 1638
- retinoic acid synthesis regulation, 1638
- alcohol dehydrogenase gene, 1638
- $\alpha 1(I)$ collagen gene
- tissue-specific expression, 2066
- transgenic mice, 2066
- upstream regulatory region, 2066
- α -globin gene cluster
- major regulatory element, 4679
- cardiac actin gene promoter
- CARG boxes, multiple, 4796
- embryonal carcinoma cells, 4796
- embryonic cardiac muscle cells, 4796
- CCG1 gene
- G₁ phase progression, 3317
- nuclear DNA-binding protein, 210 kilodalton, 3317
- CD44 gene
- neuroblastoma cells, repression of expression in, 5446
- cDNA
- BHK cell chemically transformed phenotype suppression, 5321
- chromosome 16
- G₂ mRNA, different forms, 1146
- splicing of gene transcripts, alternative, 1146
- cisplatin-resistant cell line
- UV radiation, cross-resistance to, 2075
- UV-modified DNA, overexpression of cellular factors that recognize, 2075
- colony-stimulating factor 1 receptor
- ligand-induced conformational changes, 2489
- peptide antisera, 2489
- phosphatidylinositol-3 kinase binding site, 2489
- cot oncogene
- protein kinase, putative, 4088
- structure and transforming potential, 4088
- DNA polymerase α
- sequences controlling expression in cycling and serum-stimulated cells, 2081
- double-stranded RNA modification activity, regulation of, 3719
- epidermal growth factor
- aromaticity at position 37 not obligatory for activity, 2425
- erythroleukemic cell line
- globin gene expression, negative regulation of, 3528
- megakaryocytic differentiation, 3528
- α -fetoprotein enhancer-binding protein
- ATBF1
- four homeodomains and seventeen zinc fingers, 6041
- c-fgr
- monocyte-specific enzyme induction in NIH 3T3 cells, 6279
- fibroblast growth factor
- common structural arrangement, 4627
- third immunoglobulin domain, receptor forms that differ in, 4627
- fibroblast growth factor-5 biosynthesis, 1840
- fibroblasts
- excision repair proficient, 1927
- repair-deficient cells, 1927
- strand bias, cell cycle dependent, 1927
- UV-induced mutations, 1927
- c-fos
- promoter elements, multiple basal, 1270
- transcription level, 1270
- gadd45 gene
- ionizing radiation, induction by, 1009
- protein kinase C, lack of mediation by, 1009
- γ -actin gene
- chromosome location, 3296
- evolution, 3296
- expression, 3296
- smooth muscle (enteric type), 3296
- structure, 3296
- ϵ -globin gene promoter
- GATA-1 site, conserved, transcriptional role of, 2558
- α -globin genes
- developmental regulation, autonomous, 3786
- transgenic mice, 3786
- α - and β -globin genes
- transient heterokaryons, 1239
- H3 histone mRNA
- cell cycle, changes in stability during, 544
- heat shock transcription factor
- hsp70 promoter interaction, 586
- modular recognition of 5-base-pair DNA, sequence motifs, 3504
- hepatoma
- α -fetoprotein expression, repression of, 5885
- position-dependent silencer, 5885
- histone gene transcription factor binding, 5825
- hsp70 promoter
- heat shock transcription factor interaction, 586
- hypoxanthine phosphoribosyltransferase gene
- negative regulatory element, evidence for, 4157
- interferon gamma receptor, 0
- species-specific signal transducer, interaction with, 5860
- interleukin-7 receptor gene
- mRNAs generated by differential splicing, 3052
- type I-interferon-inducible promoter, 3052
- keratinocyte autocrine factor, heparin sulfate regulated
- amphiregulin, 2547
- leukemias
- BCR/ABL tyrosine kinase oncogene, 1785
- Philadelphia chromosome positive, 1785
- leukocyte adhesion and activation anti-ger BLAST-1 (CD48)
- Epstein-Barr virus, induction by, 1614
- major histocompatibility complex class I genes
- cis sequences controlling expression, 3564
- transgenic mice, expression in, 3564
- malignant cell line
- novel pathway of mutation, 3163
- mammary carcinoma cells
- c-erbB-2/HER2 gene product phosphorylation, 979
- serum growth factors, 979
- mitochondrial DNA
- heavy-strand promoter region, lack of, 1631
- replication competent, 1631
- mitochondrial RNA processing/7-2 RNA
- To autoantigen (40 kilodalton), in vitro association, 5266
- mutant cell line
- alpha and beta interferons, unresponsiveness to, 4189
- c-myb expression
- Myb binding sites in 5' flanking region, 6166
- positive autoregulation, 6166

- c-myc promoter-binding protein, 2154
 myeloid leukemia cells, primary
axl transforming gene, 5016
 receptor tyrosine kinase, novel, 5016
 p70 S6 kinase
 two polypeptides differing only at amino termini, 5541
 platelet-derived endothelial cell growth factor gene
 chromosomal location, 2125
 organization, 2125
 preadipocytes
 adipose P2 gene expression, 2303
 C/EBP-binding region, 2303
 promoter
 Sp1, synergistic activation by, 1935
 proto-oncogene *PBX1*
PBX2 and *PBX3*, new homeobox genes with extensive homology, 6149
 replicon initiation, inhibition of topoisomerase-DNA cleavable complexes, stabilization of, 3711
 retinoblastoma protein
 family of related polypeptides, 5792
 S3 ribosomal protein
 overexpression in colorectal cancer, 3842
 small RNP
 7SK ribonucleoprotein, 3432
 T cells, CD3 stimulated
 Raf-1 expression, interleukin-2 triggered, 2794
 T-cell receptor δ enhancer
 transcriptional activation site, essential, 5671
 teratocarcinoma cells
 homeobox gene expression, alteration of, 3573
 PA-1 cells, 3573
 N-ras transformation, 3573
 thymidine kinase gene
 cell cycle regulatory unit, 2296
 Human cells
 DNA replication, autonomous
 DNA size, 2263
 DNA source, 2263
 Human immunodeficiency virus type I
 gene expression, UV-induced
 suppression at posttranscriptional level by poly(ADP-ribose) polymerase inhibitors, 3522
 long terminal repeat
 transcriptional activators, early response to, 1883
 Rev response element
 Rev-nucleolar B23 protein complex dissociation, 2567
 Rev-nucleolar B23 protein complex
 Rev response element, dissociation by, 2567
 transcription control region, 1624, N0
 long terminal repeat U3 sequences, 1624
 Human T-cell leukemia virus type I
 transactivator p40^{tax}
 gp34 glycoprotein, induction of, 1313
 Human T-cell lymphotropic virus type I
tax gene
 nerve growth factor *trans* activation, 4635
 transforming growth factor- β , overexpression of, 5222
 transgenic mice, 4635, 5222
HXT1 gene product
S. cerevisiae
 hexose transporter, 3804
 Hybrid response elements
 steroid hormone receptors, functional interaction with, 3247
 Hydrophobic protein sequence
 nuclear localization signal, override of, 5137
 Hygromycin phosphotransferase-thymidine kinase fusion gene
 dominant positive and negative selection, 3374
 Hypoxanthine phosphoribosyltransferase gene
 human
 negative regulatory element, evidence for, 4157
 Id
 helix-loop-helix transcription factor repressor
 immunoglobulin kappa 3' enhancer regulation, 1040
 Id1 and Id2 proteins
 helix-loop-helix proteins, inhibition of DNA binding by one class of, 5603
 IEF1
 β -cell-specific transcription factor, 1547
 insulin gene expression, 1547
 Immediate early response
 interleukin-6, 4371
 leukemia inhibitory factor, 4371
 Immediate-early genes
 41 novel, 381
 Immediate-early growth response
 3T3 cells
 serum stimulated, 381
 H-35 cells
 insulin stimulated, 381
 immediate-early genes
 41 novel, 381
 regenerating liver cells, 381
 Immediate-early response gene JE
 induction
 cholera toxin, 102
 cyclic AMP-independent signaling pathway, 102
 Immunoglobulin
 heavy-chain variable region gene
 5' matrix-associated region, 5206
 transcription in response to antigen plus interleukin-5
 protein-DNA interactions, novel, 5197
 Immunoglobulin D
 mouse
 J_H-C_H locus, nonhomologous recombination within, 5660
 Immunoglobulin DJ_H
 D-to-J_H rearrangement, 2096
 promoter-enhancer approximation, 2096
 transcription, 2096
 Immunoglobulin enhancer
 helix-loop-helix protein Id, repression by B-lymphoid-cell development, implications for, 6185
 Immunoglobulin gene
 regulation, positive and negative
 B-cell-specific enhancer element, novel, 75
 Immunoglobulin heavy-chain enhancer
 common factor I transcriptional activator binding, 1765
 Immunoglobulin kappa 3' enhancer
 developmental control, 1040
 helix-loop-helix transcription factor repressor, 1040
 Id, regulation by, 1040
 Immunoglobulin kappa gene
 expression, silencing of
 non-B cells, 1431
 Immunotoxins, single chain
 transferrin receptor, human
 anti-TFR(Fv)-PE40, 2200
 diphtheria toxin, 2200
 DT388-anti-TFR(Fv), 2200
Pseudomonas exotoxin A, 2200
 IMP dehydrogenase gene
 end products, regulation of expression by, 5417
 guanine nucleotides, regulation of expression by, 5417
 Inducible cytoplasmic factor (AU-B)
 lymphokine mRNA, binding to, 3288
 Influenza virus
 NS1 mRNA
 nucleocytoplasmic transport, 1092
 splicing, 1092
 Initiation factor eIF-4E mRNA
 antisense mRNA expression in HeLa cells
 cell division times, lengthened, 5435
 eIF-4E, reduced levels of, 5435
 p220 component of eIF-4E, reduced levels of, 5435
 translation rates, diminished, 5435
 Inorganic phosphate transporter
S. cerevisiae *PHO84* gene, 3229
 "In-out" targeting procedure
 mouse embryonic stem cells
 genomic modifications, 1402
ins1
S. cerevisiae
SRK1, suppression by, 3369
 Insertional mutagenesis
 retrovirus induced
 collagen mutation, mechanism of, 5154
 Mov13 mice, 5154
 Insulin gene
 pancreatic β -cell-type-specific transcription
 basic helix-loop-helix DNA-binding proteins, 1734
 Insulin gene expression
 β cells, 1547
 β -cell-specific transcription factor IEF1, 1547
 fibroblasts, 1547
 nonexpressing cells
 multiple distinct negative-acting control elements, regulation by, 2887
 Insulin-induced gene expression
 p21^{ras}, two dominant inhibitory mutants of, 5963
 Insulinlike growth factor I
 3T3 fibroblasts, 731
c-myc, abrogation of requirement by, 731
 Insulinlike growth factor-binding protein I
 gene
 rat
 induction, 1393
 regenerating liver, induction in, 1393

- Int-2/Fgf-3* oncogene product
extracellular matrix, association with
cell transformation, implications for,
5929
secretion, 5929
Integration in vitro
retrovirus, avian, 1419
Interferon
alpha and gamma
guanylate-binding protein gene pro-
moter, 182
transcriptional induction, 182
guanylate-binding proteins, induction by,
4717
Interferon gamma receptor
human
extracellular domain, 5860
species-specific signal transducer, in-
teraction with, 5860
Interferon- β , growth inhibition by
BALB/c-3T3 fibroblasts, resistant
aberrant growth factor signal transduc-
tion, 3148
Interferon- γ
c-fos mRNA downregulation at posttran-
scriptional level, 2718
Interferons
alpha and beta
unresponsive human mutant cell line,
4189
Interleukin 2
phosphatidylinositol 3-kinase activity,
modification of, 4431
Interleukin-2
Raf-1 expression
G₁ and S, increase through, 2794
Raf-1 phosphorylation
G₁ and S, increase through, 2794
Raf-1-associated kinase activity
G₁ and S, increase through, 2794
T cells, human, CD3 stimulated, 2794
Interleukin-2 promoter
mitogen-induced activation
FK-506, inhibition by, 4074
retinoic acid-induced down-regulation
cis-regulatory sequences containing
octamer motif, 4771
Interleukin-5
immunoglobulin transcription increase
protein-DNA interactions, novel, 5197
Interleukin-6
B-cell hybridoma, 1409
immediate early response
leukemia inhibitory factor, 4371
myeloid leukemia differentiation, in-
duction of, 4371
tyrosine phosphorylation, 4371
junB transcription, 1409
myeloid leukemia cell differentiation in-
duction
c-myc, block by, 2375
intermediate-stage block by *c-myc*,
2375
TIS11 gene transcription, 1409
Interleukin-7
hyperexpression
pre-B lymphoid cell line transforma-
tion, 854
Interleukin-7 receptor gene
human
mRNAs generated by differential
splicing, 3052
type I-interferon-inducible promoter,
3052
mouse
mRNAs generated by differential
splicing, 3052
type I-interferon-inducible promoter,
3052
Interleukin-7 retroviruses
pre-B cell transformation
Abelson murine leukemia virus, 1590
autocrine mechanism, 1590
Intracellular receptor function
dioxin receptor
activation to DNA-binding form, 401
receptor affinity determination, 401
ligand, role of, 401
Intracellular signaling pathways
aplatelet-derived growth factor receptor
kinase insert domain
functional coupling, effects of deletion
or substitution on, 134
Intrachromosomal rearrangements
L-myc and *rlf* fusion
small-cell lung cancer, 4015
Intracisternal A particle
long terminal repeat promoter
EBP-80, 117
methylation response, 117
transcription factor EBP-80, 117
Intracisternal A-type particle
cytokine genes, activation of
functional cytokine mRNAs, genera-
tion by retroviral splicing events,
5562
murine myelomonocytic leukemia,
5562
Intron, generic
transgenic mice
increase of gene expression, 3070
Ionizing radiation
human *gadd45* gene induction
protein kinase C, lack of mediation
by, 1009
IRA1 GTPase-activating protein, 4591
S. cerevisiae
adenylate cyclase, interactions with,
4591
Isomerase, peptidyl-prolyl *cis-trans*
S. cerevisiae
FK506-binding protein, relation to,
1718
rapamycin sensitivity, mediation of,
1718
JE gene
tumor formation, suppression of, 3125
J_H-C₈ locus
mouse
C μ deletion, 5660
immunoglobulin D secretion, switch
to, 5660
nonhomologous recombination, 5660
Jun
protein family
cell cycle progression, requirement
for, 4466
Fos, 4466
thyroid hormone receptor, interaction
with
novel pathway for action, 6016
transcriptional regulation in vitro
Fos, 3624
multiple activator and regulatory do-
mains, interaction among, 3624
c-jun
UV response, mammalian
rapid and preferential activation, 2804
Jun and Fos protein expression
G₀-to-G₁ transition
in vivo and in vitro associations, 2451
mouse fibroblasts, 2451
c-Jun proto-oncoprotein
transactivating function
cotransformation of rat embryo cells,
requirement for, 6286
jun/AP-1
E1A, positive regulation by, 192
junB
B-cell hybridoma, 1409
interleukin-6, activation by, 1409
transforming growth factor- β 1, control
by, 972
K1 killer toxin
S. cerevisiae
functional domains, mutational analy-
sis, 175
K⁺ transporters
S. cerevisiae
TRK1 and *TRK2*, structurally related,
4266
Keratinocyte autocrine factor, heparin su-
lfae regulated
human
amphiregulin, 2547
Kidney development
mouse
Wilms' tumor gene (WT1) expression,
1707
Kinase Spk1
S. cerevisiae
phosphorylation of proteins on serine,
threonine, and tyrosine, 987
Kinesin
X. laevis cDNA encoding related pro-
tein, 3395
Kit
association with cytoplasmic signaling
proteins
steel factor, induction by, 3043
autophosphorylation
steel factor, induction by, 3043
c-kit mRNA
hemopoietic growth factors, modulation
by, 2901
c-kit protein
hemopoietic growth factors, modulation
by, 2901
Kluyveromyces lactis
GAL gene induction
galactokinase encoded by *GAL1*, re-
quirement for, 5454
Krev-1 (Rap1A) protein
COOH-terminal domain
isoprenylation, 1523
transformation by H-Ras:Rap1A chi-
meric protein, support of, 1523
L16 ribosomal protein
S. cerevisiae temperature-sensitive mu-
tants, defect in, 5681
L929 fibroblasts
anchor biosynthesis, 2362
glycolipid-anchored membrane proteins,
2362

- LaBelle mitochondrial plasmid
N. intermedia
 DNA polymerase, novel, 1696
 reverse transcriptase derivation of
 DNA polymerase, 1696
- LAC9 transcription activator
 C6 zinc finger, 1777
 DNA sequence recognition
 base and backbone contacts, 1777
- Large T antigens
 papovavirus
 choroid plexus, uniform cell-autono-
 mous tumorigenesis of, 5968
- Large-T antigen
 simian virus 40
 adenovirus E1A gene products, 2116
 dephosphorylation by protein phos-
 phatase 2A, 1996
 inhibition of dephosphorylation by
 small-t antigen, 1996
 p3000-associated transforming func-
 tion, biological activity comple-
 mentary to, 2116
- Leishmania enriettii*
 histone H2B mRNAs
 structure and regulation, 240
- Lens cell transcription factor
 mouse
 γ F-crystallin promoter proximal do-
 main, interaction with, 1531
- Leucine zipper
 intracellular interactions, 954
 c-Myc hetero-oligomerization, 954
- Leucine zipper transcription factor
 vitellogenin gene-binding protein, 4863
- Leucine-rich repeat
S. cerevisiae *GRRI* protein, 5101
- Leukemia inhibitory factor
 immediate early response
 interleukin-6, 4371
 myeloid leukemia differentiation, in-
 duction of, 4371
 tyrosine phosphorylation, 4371
 myeloid leukemia cell differentiation in-
 duction
 c-myc, block by, 2375
 intermediate-stage block by c-myc,
 2375
- Leukemia, T-cell acute lymphoblastic
SIL, disruption of
 structural characterization, 5462
- Leukocyte adhesion and activation antigen
 BLAST-1 (CD48), 1614
- Leukocyte antigen MRC OX-44
 rat
 cell surface proteins, new family of,
 2864
 growth regulation, 2864
- Light, transcription repression by
 asparagine synthetase genes
 photosynthetic and nonphotosynthetic
 organs, 4966
- LIM 1215
 colon carcinoma cell line
 autocrine factors, 4005
 proliferative and morphologic re-
 sponses, 4005
- LINE-1 RNA
 mouse embryonal carcinoma cells
 ribonucleoprotein particles, 4804
- Lipids
D. discoideum
 cell-cell cohesion modulation, 468
 cyclic AMP signaling modulation, 468
- Lipopolysaccharide
 tissue factor mRNA regulation, tran-
 scriptional and posttranscriptional,
 4732
- Lipopolysaccharide-plus-interleukin-4-re-
 sponsive element
 germ line ϵ transcripts promoter, 5551
- Liver
 mouse
 glutamine synthetase gene, position-
 specific transcription, 6050
 hepatocytes, interaction with collect-
 ing (hepatic) veins, 6050
 ornithine aminotransferase gene, posi-
 tion-specific transcription, 6050
- regenerating
 insulinlike growth factor-binding pro-
 tein I gene induction, 1393
 transcription factor modulation
 extracellular matrix, 4405
 transcription factors
 differentiation, hepatic, 773
 extracellular signals, regulation by,
 773
- Liver cells
 apolipoprotein AI gene expression
 transcription factors, synergistic inter-
 actions, 677
- rat
 cytochrome P-450IA1 gene, 4314
 xenobiotic response element-binding
 factor, 4314
 xenobiotic response elements 1 and 2,
 4314
- regenerating
 immediate-early growth response, 381
- Liver, developing
 mouse
 myc family gene expression, complex
 transcriptional regulation of, 6007
- Liver-specific and cytokine-inducible nu-
 clear factor
 NF-AB
 interleukin-1 response element of rat
 α 1-acid glycoprotein gene, 3001
- Liver-type promoter
 6-phosphofructo-2-kinase/fructose-2,6-
 bisphosphatase gene
 protein-binding sites, 1099
 regulatory sequences, 1099
- LM-TK⁻ fibroblasts
 anchor biosynthesis, 2362
 glycolipid-anchored membrane proteins,
 2362
- Lovastatin
 ras activation of 12-O-tetradecanoylphorbol-13-acetate response
 element
 selective inhibition, 2307
- Lung
 PKC-L, specific expression, 126
- LyF-1
 transcriptional regulator
 lymphocyte-specific genes, interaction
 with novel class of promoters for,
 5229
- Lymphocytes
 intestinal intraepithelial
 murine athymic chimeras, 5902
 T-cell receptor gamma genes, 5902
- Lymphocyte-specific genes
 novel class of promoters
 Lyf-1 transcriptional regulator, inter-
 action with, 5229
- Lymphokine genes
 element shared by three
 nuclear factors, interaction with, 5894
- Lymphokine mRNA
 AUUUA multimers
 inducible cytoplasmic factor binding,
 3288
- Lymphoma cells
 mouse S49 cell kinase-negative mutant
 cyclic AMP-dependent protein kinase
 catalytic subunit maturation de-
 fect, 705
- Lymphoma mutants
 Thy-1 negative
 mannolipids, atypical, 3879
- lyn kinase
 21 amino-terminus amino acids, two
 forms differing by, 2391
 hematopoietic cells, two forms ex-
 pressed by, 2391
- lyn mRNAs
 mouse
 alternatively spliced, 3399
- Macronuclear genome
P. tetraurelia, 1133
- Macronuclear transformation
P. tetraurelia
 new macronuclear genome content
 control, 1133
- Macronuclei
T. thermophila
 high-mobility-group-like chromosomal
 proteins, 166
- Macrophage
 c-fos mRNA
 interferon- γ , downregulation by at
 posttranscriptional level, 2718
- mouse
 c-fos gene transcription, 2826
- Maize
Ds1 element, transposable
 alternative splicing from exon se-
 quences, 6192
- mitochondria
cox2 transcripts, RNA editing interme-
 diates, 4278
- mitochondrial gene expression
 transcriptional and posttranscriptional
 regulation, 533
- Major histocompatibility complex class I
 gene
 complex regulatory DNA element
 silencer and enhancer, 4217
- Major histocompatibility complex class I
 genes, human
 transgenic mice, expression in
cis sequences controlling expression,
 3564
 efficient position-independent tissue-
 specific expression, 3564
- Major histocompatibility complex class II
 DRA promoter function
 X and Y elements, requirement for
 stereospecific alignment of, 2406
- Major histocompatibility complex class II
 genes promoter
 CCAAT box-binding factor, 578

- Major histocompatibility complex genes, mammalian
yeast mating-type genes
regulatory mechanisms, striking similarities, 4228
- Major urinary protein gene enhancer
mouse
submaxillary gland expression, 4244
- Malate dehydrogenase
S. cerevisiae
three isozymes, evidence for, 370
- Male germ cell
calmodulin-binding protein, specific, 3960
- Malfolded proteins
grp78 promoter transactivation, 5612
- Malignant cell line, human
novel pathway of mutation, 3163
- Mammalian gene targeting reaction
double-strand gap repair, 4389
- Mammalian genomes
replication initiation sites
mapping, 3850
replication intermediates, stabilization and enrichment of, 3850
- Mammalian hexose transporter
drug resistance, development of, 3407
- Mammalian transcription factors
IIF, IIS, and IIX
RNA polymerase II, role during elongation by, 1195
- Mammalian type 2A protein phosphatase B subunit
S. cerevisiae CDC55, homology to, 5767
- Mammary carcinoma cells
human
c-erbB-2/HER2 gene product phosphorylation, 979
serum growth factors, 979
- Mammary cell lines
mouse mammary tumor virus promoter regulation, 2529
- Mammary gland-specific nuclear factor
 β -casein gene promoter activity regulation, 3745
- Mannolipids
lymphoma mutants, Thy-1 negative, 3879
- MATa1* cistron pre-mRNA splicing
S. cerevisiae
AAR2 gene, 5693
- MATa* locus
S. cerevisiae
RAP1 role in regulation of *MATa* locus, 1069
- Mating pheromone
 α -factor, *S. cerevisiae*
C-terminal cysteine modifications, 3603
- Mating pheromones
S. cerevisiae
Tyl transposition, inhibition of, 2736
- Mating-defective mutants
S. cerevisiae
SIR1 gene, extragenic suppressor by, 2253
- Mating-type genes, yeast
major histocompatibility complex genes, mammalian
regulatory mechanisms, striking similarities, 4228
- Mating-type switching
S. cerevisiae
"stuck" mutation, heteroduplex formation and mismatch repair of, 5372
- Matrix-associated region, 5'
immunoglobulin heavy-chain variable region gene, 5206
- Maturation-producing factor
Xenopus oocytes
trp-met oncogene product, activation by, 5985
- mb-1* promoter, pre-B- and B-cell-specific heterogeneously initiated transcription initiation site sequences, requirement for, 5756
upstream factor-binding sites, requirement for, 5756
- MDH2 gene
S. cerevisiae
disruption, 370
isolation, 370
nucleotide sequence analysis, 370
- mdr1*
mouse
chimeric genes, *mdr1* and *mdr2*, 595
- mdr2*
mouse
chimeric genes, *mdr1* and *mdr2*, 595
- Megabase-sized DNA
pulsed-field electrophoresis, 3348
- Meiosis
S. cerevisiae
sister chromatid exchange, genetic and physical analyses of, 6328
- Meiotic induction
X. laevis
cyclin B, 1713
mos^{3c} coexpression, acceleration by, 1713
- Meiotic recombination
S. cerevisiae
specific base-pair mismatch repair, 737
- Membrane proteins
anchor biosynthesis, 2362
glycolipid anchor, 2362
glycophospholipid anchors
dolichol-phosphoryl-mannose synthesis-blocked mutants, 391
- Merozoite surface antigen (MSA-2), 38- to 45-kilodalton
P. falciparum, 963
structural and antigenic polymorphism, 963
- Met
hepatocyte growth factor receptor
C-terminal truncated forms, 5954
- MET proto-oncogene
hepatocyte growth factor receptor, 6084
tyrosine kinase
autophosphorylation, activation by, 1793
defective posttranslational processing, activation by, 6084
- met* receptor tyrosine kinase
isoforms, generation by alternative splicing
differential processing, 2962
- Metallothionein gene
S. cerevisiae
heat shock transcription factor, 3676
- Metallothionein gene transcription
S. cerevisiae
heat shock transcription factor, activation by, 1232
- Methylation response
intracisternal A-particle long terminal repeat promoter, 117
EBP-80 transcription factor binding, 117
- Mg²⁺-binding site
Ras^H
GTP, activation by, 4822
mutations, dominant inhibitory, 4822
- Mg²⁺-binding site, putative
G_s α
activation by receptors, 4830
mutation, 4830
- Mice, transgenic
human $\alpha 1(I)$ collagen gene expression
upstream regulatory region, 2066
major histocompatibility complex class I genes, human
cis sequences controlling expression, 3564
efficient position-independent tissue-specific expression, 3564
- Microfilament binding
c-abl
bcr/abl fusion proteins, activation by, 1553
- Micronuclei
T. thermophila
high-mobility-group-like chromosomal proteins, 166
- Microtubule
D. melanogaster
 β -tubulin codon change, 4726
- Microtubule-associated protein kinase
homolog in *X. laevis* oocytes and eggs
cell cycle tyrosine phosphorylation, 1965
- Microtubule-dependent cellular processes
S. cerevisiae
CDC20 gene product, requirement for, 5592
- Microtubule-mediated processes
S. cerevisiae homolog to mouse *Tcp-1*, 2629
- Minichromosomes
T. brucei
DNA nucleotide sequence elements, 3823
- Minicircles
T. equiperdum
guide RNA, 1668
transcripts, three distinct primary, 1668
- Minute virus of mice attenuator
block to transcription elongation
cellular elongation factors, regulation by, 3515
- Mismatch repair
S. cerevisiae
"stuck" mutation, 5372
- Mismatches, G-A or C-T
correction to G-C pairs
S. cerevisiae *rad18* mutator, 218
- Mitochondria
C. (Torulopsis) glabrata
RNase P activity, 1662
cytochrome *c* import and accumulation
S. cerevisiae cytochrome *c* heme lyase, 5487

- maize
 cox2 transcripts, RNA editing intermediates, 4278
 transcriptional and posttranscriptional regulation of gene expression, 533
 mitochondrial DNA-less cells, 2236
 myopathy patient
 protein synthesis and respiration defects, in vitro genetic transfer of, 2236
P. hybrida
 cis- and *trans*-splicing, pre-mRNA editing before, 4274
 pre-mRNA editing before *cis*- and *trans*-splicing, 4274
 pre-mRNA editing before *cis*- and *trans*-splicing, 4274
S. cerevisiae
 α -ketoglutarate dehydrogenase complex, 3931
 Mitochondrial DNA
 human
 heavy-strand promoter region, lack of, 1631
 replication competent, 1631
 Mitochondrial DNA-less cells, 2236
 Mitochondrial function, induction of
 S. cerevisiae
 CBP1, 813
 mRNA 3' end formation, 813
 Mitochondrial gene, plant
 transcription, accurate in vivo, 2035
 Mitochondrial genes
 S. cerevisiae
 COX1 and *COX3*, facilitation of, 2399
 Mitochondrial import
 S. cerevisiae
 temperature-sensitive defect, 2647
 Mitochondrial RNA processing/7-2 RNA
 human
 To autoantigen (40 kilodalton), in vitro association, 5266
 Mitochondrial rRNA
 T. brucei
 posttranscriptional 3' polyuridine tail formation, 5878
 Mitochondrial tRNA
 N⁶-isopentenyladenosine modification, 2382
 Mitochondrial uncoupling protein gene
 transgenic mice
 brown fat, 4147
 DNase I hypersensitivity, 4147
 Mitogen-activated protein kinase
 3T3 cell variant
 tetradecanoyl phorbol acetate, mitogenically nonresponsive to, 1002
 regulation, defective, 1002
 Mitogenesis
 tyrosine phosphorylation induced by erythropoietin receptor, correlation with, 4895
 Mitosis
 thymidine kinase degradation, 2538
 Mitotic chromosome separation
 S. cerevisiae
 centromere CDEIII sequence, 5212
 Mitotic control
 S. pombe *dis3⁺* gene, 5839
MOD5
 S. cerevisiae
 N⁶-isopentenyladenosine modification of tRNA, 2382
 translation initiation sites, 2382
 Modular recognition of 5-base-pair DNA sequence motifs
 heat shock transcription factor, human, 3504
 Moloney murine leukemia virus
 insertional mutagenesis, induction of collagen mutation, mechanism of, 5154
 Mov13 mice, 5154
 primer-binding site
 stem cell-specific silencer, 1214
 Monocyte-specific enzyme
 c-fgr, induction by
 NIH 3T3 cells, 6279
 Morphogenesis, cellular
 S. cerevisiae
 CDC55, 5767
 Morphogenesis genes
 S. cerevisiae
 mutants, synthetic lethal and multicopy suppressor, 1295
c-mos
 oocytes, mouse
 initiator-related sequences, control by, 5190
 transcription initiation site, 5190
mos gene
 transforming efficiency
 cytostatic factor activities, correlation with, 604
 oocyte maturation, correlation with, 604
v-mos
 mouse fibroblasts
 α B crystallin accumulation, 803
 NIH 3T3 fibroblasts
 α B crystallin accumulation, 803
 Ha-ras expression, 803
mos^{Xe}
 X. laevis meiotic induction
 cyclin B coexpression, 1713
 Mouse
 adenosine deaminase gene exon 1
 premature 3' end formation in a cell-free transcription system, 5398
 α B-crystallin gene
 lens and skeletal muscle, expression in, 4340
 muscle-preferred enhancer, 4340
 β -glucuronidase gene
 androgen responsiveness, 5426
 haplotype-specific sequence diversity within intron 9, 5426
 nuclease hypersensitivity within intron 9, 5426
 protein binding within intron 9, 5426
 β -major-globin gene
 erythroid differentiation, derepression of transcription during, 4324
 brain, developing
 myc family gene expression, complex transcriptional regulation of, 6007
 CD4 gene
 T-cell-specific enhancer, 5506
 chimeric genes
 mdr1 and *mdr2*, exchange of homologous domains, 595
 chromosome 1
 homogeneously staining region, inherited, 2229
 E β meiotic recombination hot spot
 DNase I-hypersensitive sites, 1813
 transcription factor-binding motifs, 1813
 embryonal carcinoma cells
 LINE-1 RNA, 4804
 ribonucleoprotein particles, 4804
 embryonic stem cells
 cotransformation, 2769
 gene targeting, 2769
 genomic modifications, "in-out" targeting procedure for, 1402
 E μ -*myc* transgene
 pre-B-cell leukemia, prenatal, 1176
 E μ -*pim-1* transgene
 pre-B-cell leukemia, prenatal, 1176
 erythroleukemia cell line
 erythropoietin receptor gene, unregulated expression of, 5527
 Evi-1 zinc finger proto-oncogene
 DNA-binding protein, sequence specific, 2665
 fibroblast cells
 G α -to-G β transition, 4943
 NF- κ B DNA-binding activity, induction of, 4943
 fibroblasts
 G α -to-G β transition, 2451
 Hox-2.4 homeobox gene activation, oncogenic potential, 554
 Jun and Fos protein expression, 2451
 c-fos gene
 transcription arrest, premature, sequence requirements for, 2832
 γ F-crystallin promoter
 lens cell transcription factor, interaction with, 1531
 proximal domain, 1531
 granulocyte-macrophage colony-stimulating factor
 lymphokine gene element, nuclear factors that interact with, 5894
 nuclear factors, lymphokine gene element interaction with, 5894
 hck
 subcellular localization, 4363
 two isoforms, 4363
 histone genes
 transcriptional activator, common, 2929
 histone H2a gene
 histone 3'-processing site, intact, 497
 transcription termination, 497
 interleukin-7 receptor gene
 mRNAs generated by differential splicing, 3052
 type I-interferon-inducible promoter, 3052
 J μ -C δ locus
 C μ deletion, 5660
 immunoglobulin D secretion, switch to, 5660
 nonhomologous recombination, 5660
 kidney development, 1707
 L929 fibroblasts
 anchor biosynthesis, 2362
 glycolipid-anchored membrane proteins, 2362
 liver
 glutamine synthetase gene, position-specific transcription, 6050
 hepatocytes, interaction with collecting (hepatic) veins, 6050
 ornithine aminotransferase gene, position-specific transcription, 6050
 liver, developing

- myc* family gene expression, complex transcriptional regulation of, 6007
 LM-TK⁻ fibroblasts
 anchor biosynthesis, 2362
 glycolipid-anchored membrane proteins, 2362
lyn mRNAs
 alternatively spliced, 3399
 macrophage
 c-fos gene transcription, 2826
 major urinary protein gene enhancer
 submaxillary gland expression, 4244
mdr1 gene
 chimeric genes, *mdr1* and *mdr2*, 595
mdr2 gene
 chimeric genes, *mdr1* and *mdr2*, 595
 myelomonocytic leukemia
 cytokine gene activation by intracisternal A particles, 5562
 functional cytokine mRNAs, generation by retroviral splicing events, 5562
 oocytes
 c-mos, control of expression by initiator-related sequences, 5190
 plasmacytoma induction
 c-myc proto-oncogene locus DNA repair, 3095
 pre-B-cell leukemia, prenatal, 1176
Ras
 GTPase-activating protein, 2785
 phospholipids, mitogenically active, 2785
n-ras
 negative regulatory element, 1334
 promoter, 1334
 upstream regulatory sequences, 1334
 rRNA processing, primary
 RNA structural motifs, 458
 sequence organization, 458
 S49 lymphoma cells
 cyclic AMP-dependent protein kinase catalytic subunit maturation defect, 705
 kinase-negative mutant, 705
 Sp1 expression, developmental, 2189
Surf-1 and *-2* genes
 bidirectional promoter, 1281
Tcp-1
 microtubule-mediated processes, 2629
 S. cerevisiae homolog, 2629
Thy-1 gene promoter
 functional domains, 2216
 thymidylate synthase gene
 5'-flanking region, 1023
 growth-stimulated cells, 1023
 tissue plasminogen activator promoter
 GC box-binding activity in brain, 3139
 no GC box-binding activity in kidney and liver, 3139
 transforming growth factor- β 1 promoter
 characterization, 84
 Ha-ras oncogene, activation by, 84
 tumor necrosis factor
 type I and type II receptors, 3020
 Wilms' tumor gene (WT1), 1707
 zona pellucida activity
 oocyte-specific factors binding to conserved upstream sequence, 6197
 Mouse cells
 chromatid interactions
 direct-repeat analysis, 4839
 recombination, intrachromosomal, 4839
 Mouse mammary tumor virus
 long terminal repeat
 promoter regulation in mammary cell lines, 2529
 Mouse mammary tumor virus promoter
 derepression
 correlation with inhibition of chromatin assembly, 5259
 X. laevis oocytes, 5259
 transcription factor access
 nucleosomes, accurately positioned, 688
 Mouse NIH 3T3 fibroblasts
 v-mos expression
 α B crystallin accumulation, 803
 Ha-ras expression
 α B crystallin accumulation, 803
 Mouse, transgenic
 central nervous system
 demyelination, 5479
 GTP-binding protein gene, 886
 provirus integration, 886
 Mov13 fibroblasts
 collagen I gene
 DNA methylation, absence of, 47
 retrovirus-induced interference, 47
 Mov13 mice
 collagen mutation, mechanism of, 5154
 insertional mutagenesis
 retrovirus induced, 5154
 MRF4
 target gene specificity
 DNA-binding domain, domains outside of, 6103
 mRNA
 3' end formation
 S. cerevisiae CBP1, 813
 mRNA, developmentally regulated
 X. laevis
 degradation control, 3115
 mRNA start site selection
 S. cerevisiae
 RNA polymerase II, mutations in conserved region of, 5781
 mRNA synthesis
 heparin regulation, 108
 hormonal regulation, 108
 mRNA translation
 transforming growth factor- β 3
 inhibition by 5' untranslated region, 4306
 mRNA-binding protein
 RNA-binding domains
 RNA-binding activities, different, 3419
 mRNAs, rapidly degraded
 3' untranslated regions
 protein binding to AU-rich domains, 3355
 MSA-2
 P. falciparum
 structural and antigenic polymorphism, 963
 μ mRNA
 membrane versus secreted form
 cleavage-polyadenylation efficiency, increase in, 2324
 developmentally regulated shift, 2324
 splicing efficiency, no change in, 2324
 Multicopy suppressor mutants
 S. cerevisiae
 morphogenesis, two new genes involved in, 1295
 Multidrug resistance gene
 P. falciparum *pfmdr1*
 amplification as the result of multiple independent events, 5244
 Multidrug resistance genes
 D. melanogaster
 homologs, 3940
 Murine athymic chimeras
 lymphocytes, intestinal intraepithelial
 T-cell receptor gamma genes, 5902
Mus musculus, 2229
 Muscle
 troponin I gene, specific expression of
 helix-loop-helix muscle regulatory factors, 267
 transcription factors, ubiquitous, 267
 Muscle function
 D. melanogaster
 tropomyosin expression, small differences in, 6337
 Muscle gene elements
 single-stranded-DNA-binding proteins, interaction with, 1944
 Muscle-specific gene expression
 myosin light chain enhancer
 factor-binding site shared with skeletal actin promoter, 3735
 skeletal actin promoter
 factor-binding site shared with myosin light chain enhancer, 3735
 Muscle-specific gene products, 4854
 Muscle-specific gene transcription
 postmitotic quail myotubes, 3331
 pp60^{v-src} reactivation, repression by, 3331
 Muscle-specific intron enhancer
 D. melanogaster
 tropomyosin I gene regulation, 1901
 Mutation, novel pathway of
 malignant human cell line, 3163
c-myc
 3T3 fibroblasts, constitutive expression in
 insulinlike growth factor 1, abrogation of requirement for, 731
c-myc expression
 positive autoregulation
 Myb binding sites in 5' flanking region, 6166
c-myc proto-oncogene
 activation
 protein truncation, requirement for, 3987
c-myc
 depletion with specific antisense sequences
 ras-transformed phenotype reversal in NIH 3T3 cells, 3699
 hetero-oligomerization, 954
 leucine zipper interactions, intracellular, 954
 mRNA stability
 A+U-rich element RNA-binding factor, regulation in vitro by, 2460
 MyoD inhibition, 2842
 myogenin-initiated myogenic differentiation, inhibition of, 2842
 neu-induced transformed morphology reversal, 354
 premature termination
 HeLa nuclear extract, 4599
 RNA polymerase II transcription, 4599

- progestins, increase in expression by, 5032
 transcriptional repression, 354
 transcriptional suppression of cellular gene expression, 2291
myc family gene expression
 mouse
 brain and liver, developing, 6007
 transcriptional regulation, complex, 6007
myc family genes
 canary
 structure and expression, 1770
myc gene, endogenous
 down-regulation, mechanism of
 E μ -*myc* tumors, 440
L-myc
 rfl fusion
 intrachromosomal rearrangements, 4015
 small-cell lung cancer, 4015
N-myc
 episome-generated antisense RNA
 differentiation of primitive neuroectodermal cell lines, restriction of, 1360
 c-myc promoter
 common factor 1 transcriptional activation binding, 1765
 c-myc promoter-binding protein
 human, 2154
 c-myc proto-oncogene locus
 DNA repair
 plasmacytoma induction, 3095
 E μ -*myc* tumors
 myc gene, endogenous
 down-regulation, mechanism of, 440
 Myeloid leukemia cell differentiation
 interleukin-6, induction by
 intermediate-stage block by *c-myc*, 2375
 leukemia inhibitory factor, induction by
 intermediate-stage block by *c-myc*, 2375
 Myeloid leukemia cells, primary
 human
 axl transforming gene, 5016
 receptor tyrosine kinase, novel, 5016
 Myeloid transforming gene
 Evi-1
 retroviral insertions, 1820
 transcription activation, 1820
 Myelomonocytic leukemia
 mouse
 cytokine gene activation by intracisternal A particles, 5562
 functional cytokine mRNAs, generation by retroviral splicing events, 5562
 Myoblasts
 replicating
 α -actin gene transcription, 5090
 Myocardial cells, rat
 cardiac myosin light-chain-2 gene
 expression, 2273
 Myocyte
 E2-box-binding factors
 E12/E47-like subunits, 1156
 Myocyte-specific enhancer-binding factor
 MEF-2
 myogenin, induction by, 4854
 MyoD
 induction
 v-ski, transformation-defective, 1167
 c-myc, inhibition by, 2842
 Myofibrillar genes
 skeletal myotubes, chick
 differentiation program, 4473
 phorbol esters, selective and reversible inhibition by, 4473
 Myogenesis
 transforming growth factor- β
 secretion, 3795
 transcriptional regulation, 3795
 Myogenic cell line
 dihydrofolate reductase synthesis rates
 terminal differentiation, 3726
 Myogenic helix-loop-helix regulatory factors
 heterodimers
 binding to element governing myogenic induction, 2439
 Myogenin
 consensus binding site
 cyclic amplification and selection of targets (CASTing), 4104
 E2A products, dependence for efficient DNA binding, 3633
 homooligomerization, inefficient, 3633
 induction
 v-ski, transformation-defective, 1167
 myocyte-specific enhancer-binding factor
 MEF-2 induction, 4854
 myogenic differentiation
 c-myc, inhibition by, 2842
 target gene specificity
 DNA-binding domain, domains outside of, 6103
 Myopathy patient
 mitochondria
 protein synthesis and respiration defects, in vitro genetic transfer of, 2236
 mitochondrial DNA-less cells, 2236
 Myosin light chain enhancer
 muscle-specific gene expression
 factor-binding site shared with skeletal actin promoter, 3735
 Myosin light-chain 2 gene, cardiac
 chicken, 1676
 tissue-specific transcription, 1676
 upstream repressor element, regulation by, 1676
 Myotube formation
 v-ski, transformation-defective, 1167
 Myotubes, quail
 muscle-specific gene transcription
 pp60^{v-src} reactivation, repression by, 3331
N⁶-Isopentenyladenosine modification
 cytoplasmic tRNA, 2382
 mitochondrial tRNA, 2382
 NAD-linked glutamate dehydrogenase
 S. cerevisiae
 GDH2 gene complex upstream region
 role in nitrogen regulation, 6229
 Natriuretic peptide receptor genes
 primate tissues
 differential regional expression, 3454
 Nerve growth factor
 transgenic mice
 human T-cell lymphotropic virus type 1 *tax* gene, 4635
 trans activation, 4635
 VGF gene induction, 2335
 Nerve growth factor-induced differentiation
 v-src-induced neurite outgrowth, 4739
 Nervous system-specific mRNA
 VGF gene
 nerve growth factor, induction by, 2335
neu
 c-myc, 354
 transformed morphology induction
 reversal by *c-myc*, 354
 transcriptional repression, 354
neu oncogene
 adenovirus type 5 E1A gene products
 transformation suppressors, 1745
neu promoter
 rat
 enhancer, novel, 1875
 Neural cell adhesion molecule mRNA
 27 alternatively spliced forms, 1654
 rat heart development, 1654
 Neural retina, embryonic
 v-src expression, effects of, 5275
 Neurite outgrowth
 v-src, induction by
 nerve growth factor-induced differentiation, mimicking of critical aspects of, 4739
 Neuroblastoma
 transgenic mice
 prostate gland, restriction to, 4518
 Neuroblastoma cells
 CD44 gene
 repression of expression, 5446
 Neuroectodermal cell lines, primitive
 differentiation, restriction of
 episome-generated *N-myc* antisense RNA, 1360
 N-myc, 1360
 Neurofibromatosis type 1 gene
 oligodendrocyte-myelin glycoprotein gene, 906
Neurospora crassa
 bZIP DNA-binding protein CPC1
 aligned heptad leucines for dimerization, lack of requirement for, 935
 clock-controlled genes
 transcriptional regulation, 558
 CPC1, 935
 cpc-1 gene
 differential expression during asexual life cycle, 928
 CY53 regulatory protein
 DNA-binding domain, mutational analysis of, 4356
 cyt-20
 second function in addition to protein synthesis, 4022
 valyl-tRNA synthetases, cytosolic and mitochondrial, 4022
nir-4
 binuclear zinc DNA-binding domain,
 protein with, 5735
 pathway-specific regulatory gene, 5735
Neurospora intermedia
 LaBelle mitochondrial plasmid
 DNA polymerase, novel, 1696
 reverse transcriptase derivation of
 DNA polymerase, 1696

- Newt**
satellite 2 transcripts
self-cleavage by using extended hammerhead structure, 6109
- NF-AB**
liver-specific and cytokine-inducible nuclear factor
interleukin-1 response element of rat α 1-acid glycoprotein gene, 3001
- NF-AT1** isolated enhancer element
mitogen-induced activation
FK-506, inhibition by, 4074
- NF-1**
ras effector domain mutant interactions, 3132
- NFIL-2A** isolated enhancer element
mitogen-induced activation
FK-506, inhibition by, 4074
- NF- κ B**
activation, short and long term, 259
activity dependence
external stimuli, continuous presence of, 259
protein synthesis, 259
cyclic AMP-independent activation
HL60 cells, 2315
tumor necrosis factors α and β , 2315
 G_i -to- G_q transition
DNA-binding activity, induction of, 4943
mouse fibroblasts, 4943
- NGFI-C** early response gene
zinc finger transcriptional activator, 3835
GCCGGGGCG (GSG) element-binding protein family member, 3835
- Nicotine**
ethanol
coinduction of mammalian stress proteins HSP70 and HSP28, 6034
heat
coinduction of mammalian stress proteins HSP70 and HSP28, 6034
- NIH 3T3 cells**
monocyte-specific enzyme
c-fgr, induction by, 6279
ras transformation
c-myc, reversal of phenotype by depletion of, 3699
- nirA***
A. nidulans
four introns in highly conserved regions, 5746
GALA-type zinc finger protein, 5746
nitrate assimilation, 795
nitrate assimilation pathway-specific gene, 5746
- nit-4***
N. crassa
binuclear zinc DNA-binding domain, protein with, 5735
pathway-specific regulatory gene, 5735
- Nitrate assimilation**
A. nidulans
nirA, 795
nirA pathway-specific gene, 5746
- Nitrogen catabolic genes**
DAL81 gene product, 1161
S. cerevisiae, 1161
- Nitrogen catabolism**
S. cerevisiae
DAL80 gene, 6205
- Nitrogen regulatory gene, positive**
S. cerevisiae
GLN3, 6216
- Nitrogen source**
cellular response
S. cerevisiae URE2 gene product, 822
- N(T)KXD consensus motif**
guanylate-binding proteins, interferon induced
lack in, 4717
- Non-B cells**
immunoglobulin kappa gene silencing, 1431
- Nonerythroid cells**
globin promoter *trans*-activation, 843
- NS1 mRNA**
influenza virus
nucleocytoplasmic transport, 1092
splicing, 1092
- Nuclear division**
S. cerevisiae
protein synthesis requirements, 3691
- Nuclear DNA-binding protein**
CCGI gene, human
210 kilodalton, 3317
- Nuclear factor**
negative acting
 α -actin gene transcription, 5090
- Nuclear factor I**
binding sites
chimeric promoter, in vivo stimulation of, 2946
collagen α 1(I) promoter, murine
interaction with, 4065
Sp1 interaction with, 4065
- Nuclear factor CREB**
cyclic AMP-responsive gene induction, 1759
- Nuclear factor κ B**
T lymphocytes
proenkephalin transcription activation, 1017
zinc finger motif, binding-site recognition through
angiotensinogen gene-inducible enhancer-binding protein 1, 2887
large nuclear proteins, new family of, 2887
- Nuclear factors**
interaction with element shared by three lymphokine genes, 5894
- Nuclear localization signal**
override by hydrophobic protein sequence independently of protein context, 5137
- Nuclear phosphoprotein, stable**
E1A-associated 300-kDa product
cell cycle phase-specific modification, 5389
- Nuclear ribonucleoprotein particle**
core proteins A2 and B1
(A2)₃B1 tetramers, 864
- Nuclear RNase P**
RPRI, 721
S. cerevisiae, 721
- Nucleocytoplasmic partitioning**
rat *AMPD1* gene
alternative transcript production, 5356
- Nucleocytoplasmic transport**
influenza virus NS1 mRNA, 1092
- Nucleolar B23 protein-Rev complex**
Rev response element, dissociation by, 2567
- Nucleosomes**
mouse mammary tumor virus promoter
transcription factor access mediation, 688
transfer from parental to replicated chromatin, 6257
- Nucleotide binding domains 1 and 2, putative**
cystic fibrosis transmembrane conductance regulator
mutations, paired variants bearing, 3886
- Nur77**
PC12 cells
differential modification upon membrane depolarization and growth factor treatment, 3239
- O⁶-methylguanine-DNA methyltransferase gene**
mammalian cells, induction in
DNA-damaging treatments, 4660
- Oct-1 transcription factor**
hepatitis B virus promoter
transcription activation, 1353
HNF-1 liver-specific factor, 1353
- Oct-2**
B-cell and neuronal forms
DNA-binding specificity and functional activity, differences in, 3925
pre-B-cell differentiation
regulation, 4885
stage-specific function, possible, 4885
- Octamer-binding protein Oct-2**
B-cell and neuronal forms
DNA-binding specificity and functional activity, differences in, 3925
- Octamer-binding-like promoter elements**
 β B1-crystallin gene, chicken, 1488
- Oligodendrocyte-myelin glycoprotein gene**
neurofibromatosis type 1 gene, 906
- Oncogene-responsive sequences**
c-fos promoter
cell-specific regulation, 5381
- Oncogenic activity, regulation of**
src protein, cellular
correct spacing between kinase domain and Tyr-527, 5832
- Oocyte maturation**
mos gene
transforming efficiency, correlation with, 604
protein kinases, homologous, activation of, 2517
tyrosine phosphorylation, 2517
- Oocytes**
mouse
c-mos, control of expression by initiator-related sequences, 5190
X. laevis
chromatin assembly, inhibition of, 5259
mouse mammary tumor virus promoter derepression, 5259
- Oocyte-specific factors**
zona pellucida promoter activity, mouse
conserved upstream sequence, binding of, 6197
- ORF2-ORF3 intron, P element**
germ line-specific splicing
cis-acting sequence, 1538

- oriP* family of tandem repeats
Epstein-Barr virus
EBNA-1, role in arresting replication forks, 6268
- Ornithine aminotransferase gene
position-specific transcription
hepatocyte interaction with collecting (hepatic) veins, 6050
mouse liver, 6050
- Osmotic stability gene
S. cerevisiae, 4235
- Osteoblast
enriched cultures
activin-A binding, 250
fetal-rat parietal bone, 250
- Oxidative stress
resistance
augmentation by bovine superoxide dismutase in *D. melanogaster*, 632
- P1* gene
D. melanogaster
ecdysone, induction by, 2913
regulatory elements, transformation mapping of, 2913
- p21
c-ras^H, transformation by
critical amino acids, 6026
v-ras^H, transformation by
noncritical amino acids, 6026
- p21^{ras}
insulin-induced gene expression
dominant inhibitory mutants, two, 5963
- p21^{ras} GTPase-activating protein
protein-tyrosine kinases, regulation by activity, 1804
phosphorylation, 1804
protein interactions, 1804
subcellular distribution, 1804
- p34^{cdc2}
X. laevis oocytes and eggs
cell cycle tyrosine phosphorylation, 1965
- p34^{cdc2} phosphorylation
transforming growth factor β 1, inhibition by
G1/S-phase growth arrest, 1185
- p40^{tax} transactivator
human T-cell leukemia virus type I
gp34 glycoprotein, induction of, 1313
- p53
complexes, wild type and mutant, 12
expression
p53-negative tumor cell growth, 1
mutant tumor suppressor alleles
ras-induced cell cycle growth arrest, release of, 1344
RNA binding
covalent linkage, stable, 1598
simian virus 40 transformation
initiation and maintenance, block of, 3472
temperature-sensitive mutant
induction of growth arrest, 582
nuclear localization, increased, 582
stability, decreased, 582
- p53 mutants
transcriptional activity, 6067
- p53 protein
simian virus 40
dephosphorylation by protein phosphatase 2A, 1996
inhibition of dephosphorylation by small-t antigen, 1996
- p59^{v-rel}
transformation
protein kinase A recognition sequence, structural link to, 5867
- p60^{src}
phosphatidylinositol, association with, 1972
- p60^{v-src}
cellular matrix, detergent insoluble
association, prevention of by SH2 domain deletions, 1207
SH2 domain
deletions, 1207
- p68
double-stranded RNA, activation by, 5497
functional expression, 5497
interferon induction, 5497
RNA binding analysis, 5497
- p68 RNA helicase
nucleolar form, 1326
related genes
conserved intron, 1326
yeasts, 1326
- p68^{c-rel}
cytoplasmic retention
protein kinase A recognition sequence, structural link to, 5867
- p70 S6 kinase
human
two polypeptides differing only at amino termini, 5541
- p3000-associated transforming function
adenovirus E1A gene products
simian virus 40 large-T antigen, complementary biological activity of, 2116
- P element ORF2-ORF3 intron
germ line-specific splicing
cis-acting sequence, 1538
- PA-1 human teratocarcinoma cells
N-ras transformation, 3573
homeobox gene expression, alteration of, 3573
- Pancreas-specific gene sequences
somatic cell hybrids
transactivation in, 4423
- Pancreatic β cell
insulin gene transcription
basic helix-loop-helix DNA-binding proteins, 1734
- Papovavirus
large T antigens
choroid plexus, uniform cell-autonomous tumorigenesis of, 5968
- Paramecium tetraurelia*
new macronuclear genome content
macronuclear transformation with specific DNA fragments, control by, 1133
- PBX2 and PBX3
homeobox genes, new
human proto-oncogene *PBX1*, extensive homology to, 6149
- PC12 cells
Nur77
differential modification upon membrane depolarization and growth factor treatment, 3239
- VEGF gene
nerve growth factor, induction by, 2335
- PEP3
S. cerevisiae
vacuolar biogenesis, requirement for, 5801
- Permeabilized cells
heat shock factor
Ca²⁺, 3365
multistep activation, 3365
- Peroxisomal protein genes
positive regulation of transcription
S. cerevisiae ADR1 gene, 699
- Peroxisomes
S. cerevisiae
catalase A import, 510
immunofluorescence analysis, 510
- PET34 gene product
S. cerevisiae
COX1 mitochondrial gene, 2399
COX3 mitochondrial gene, 2399
functional domains, different, 2399
mitochondrial gene facilitation, 2399
- petD mRNA
spinach chloroplast
chloroplast proteins, specific in vitro binding to, 4380
- Petunia hybrida*
mitochondria
cis- and *trans*-splicing, pre-mRNA editing before, 4274
pre-mRNA editing before *cis*- and *trans*-splicing, 4274
- pfmdr1 multidrug resistance gene
P. falciparum
amplification as the result of multiple independent events, 5244
- Pheromone response elements
S. cerevisiae
FUS1 gene transcription, 2952
- Philadelphia chromosome
BCR/ABL tyrosine kinase oncogene, 1785
leukemias, human, 1785
-positive and -negative cell lines
BCR promoter, 1854
- PHO4
S. cerevisiae positive regulatory factor
PHO8 *cis*-acting sequence, interaction with, 785
- PHO8
S. cerevisiae
cis-acting sequence interaction with PHO4 protein, 785
- PHO84 gene
S. cerevisiae
inorganic phosphate transporter, 3229
- Phorbol ester-mediated signal transduction
pp90^{rk} phosphorylation, regulation of, 1861
S6 phosphotransferase activity, regulation of, 1861
- Phorbol esters
skeletal myotubes, chick
differentiation program, 4473
myofibrillar gene inhibition, selective and reversible, 4473
- Phosphatase, okadaic acid sensitive
cyclin degradation pathway
eggs, amphibian, 1171

- Phosphatidylcholine
type D phospholipase-mediated hydrolysis
v-Src diacylglycerol level increase, 4903
- Phosphatidylinositol-3 kinase
activation
abl oncogene variants, 1107
 α platelet-derived growth factor receptor associated activity, 3780
binding and phosphorylation
colony-stimulating factor-1 receptor tyrosine-706 and -807 phosphorylation site mutants, 4698
colony-stimulating factor 1 receptor, binding site on, 2489
pp60^{src}, association with
modification, requirement for, 1972
platelet-derived growth factor receptor phosphotyrosine-containing receptor sequence, binding through, 1125
- T lymphocytes
interleukin 2, modification of activity by, 4431
polyomavirus middle T antigen, modification of activity by, 4431
- Phosphoenolpyruvate carboxykinase gene promoter
retinoic acid response element
retinoic acid binding, 5164
thyroid hormone receptor binding, 5164
- Phospholipase C- γ
erbB-2 mitogenic signaling pathway
erbB-2 mitogenic potency, 2040
tyrosine phosphorylation, 2040
- Phospholipase C- γ 1 SH2 domain
tyrosine-phosphorylated carboxy-terminal peptide of fibroblast growth factor receptor, binding to, 5068
- Phospholipases C- γ 1 and C- γ 2
platelet-derived growth factor, 2018
- Phospholipids, mitogenically active
Ras GTPase-activating protein, association with, 2785
- Phosphomevalonate kinase gene
S. cerevisiae
ERG8, 620
- Phosphotransferase-related catalytic domain
protein kinase, new class, 2057
protein-tyrosine kinases, two novel, 2057
- Phosphotyrosine-containing proteins
v-crk oncogene product
association with, domains sufficient for, 1607
- Physarum polycephalum*
telomere-binding protein, 2282
- Pituitary
pro-opiomelanocortin gene expression
regulatory elements, synergistic interactions of, 3492
- PKC-L
protein kinase C-related gene family member, 126
specific expression in lung, skin, and heart, 126
- Plant mitochondrial gene
transcription, accurate in vivo, 2035
- Plants
asparagine synthetase genes
photosynthetic and nonphotosynthetic organs, 4966
transcription repression by light, 4966
- Plasmacytoma induction
mice
c-myc proto-oncogene locus DNA repeat, 3095
- Plasmid, autonomously replicating
human cells
replication initiation at multiple sites, 1464
- Plasmid DNA microinjection into *X. laevis* embryos
DNA compartmentalization, 299
replication efficiency, 299
- Plasmid-based system
mammalian cell gene rearrangements, study of, 3915
- Plasmodium falciparum*
merozoite surface antigen (MSA-2), 38- to 45-kilodalton
structural and antigenic polymorphism, 963
MSA-2, 963
pfmdr1 multidrug resistance gene
amplification as the result of multiple independent events, 5244
- Platelet factor 4 gene
rat
enhancer/silencer domain interaction with GATA site, 6116
transcriptional regulation, 6116
- Platelet-derived endothelial cell growth factor gene
human
chromosomal location, 2125
organization, 2125
- Platelet-derived growth factor
disulfide-linked dimerization of receptor, induction of, 3756
phospholipases C- γ 1 and C- γ 2, increase in in vivo activity of, 2018
rhoB gene induction, 3682
- α Platelet-derived growth factor
mitogenic and chemotactic signal transduction, 3780
receptor kinase insert domain deletion, 134
intracellular signaling pathways, functional coupling with, 134
substitution, 134
tyrosine mutations, 3780
receptor-associated phosphatidylinositol-3 kinase activity
abrogation of, 3780
- Platelet-derived growth factor (PDGF) receptor
disulfide-linked dimerization
induction by PDGF, 3756
phosphatidylinositol-3 kinase binding, 1125
phosphotyrosine-containing receptor sequence, 1125
- Platelet-derived growth factor receptor
stimulation
pp60^{src} substrate, 120 kilodalton
tyrosine phosphorylation, 713
- Po promoter
Tst-1 binding, 1739
- Poly(ADP-ribose) polymerase inhibitors
human immunodeficiency virus type 1
gene expression, UV-induced
suppression at posttranscriptional level, 3522
- Poly(A) site-processing factors
pre-mRNA cleavage, efficiency of, 2432
pre-mRNA recognition, 2432
- Poly(dA · dT) tract
S. cerevisiae ARG4 locus recombination
initiation site component, 322
- Polyadenylation signals
multiple inefficient
complex transcription unit, splice site choice in, 5291
- Polyadenylation sites, different classes
S. cerevisiae, 3060
- Poly(A)-binding protein
RNA-binding domains
RNA-binding activities, different, 3419
- Polycistronic pre-mRNA maturation
T. brucei
hsp70 locus, 3180
poly(A) addition, 3180
trans splicing, 3180
- Polyomavirus enhancer-like elements
 β B1-crystallin gene, chicken, 1488
- Polyomavirus middle T antigen
phosphatidylinositol 3-kinase activity, modification of, 4431
- Polyomavirus middle-T-antigen-transformed cells
pp60^{src} substrate, 120 kilodalton
tyrosine phosphorylation, 713
- Polyuridine 3' tail formation, posttranscriptional
T. brucei mitochondrial rRNA, 5878
- POU domain gene family
Tst-1
cell surface adhesion molecule Po promoter, binding to, 1739
Po promoter binding, 1739
- pp60^{src}
epidermal growth factor stimulation, 945
GTPase-activating protein
tyrosine-phosphorylated cellular proteins, induction of association with, 945
novel cytoskeleton-associated substrate, 5113
tyrosine-phosphorylated cellular proteins
GTPase-activating protein, induction of association with, 945
- pp60^{src} substrate, 120 kilodalton
tyrosine phosphorylation
epidermal growth factor receptor stimulation, 713
platelet-derived growth factor receptor stimulation, 713
polyomavirus middle-T-antigen-transformed cells, 713
- pp60^{v-src}
reactivation
muscle-specific gene transcription, repression of, 3331
postmitotic quail myotubes, 3331
- pp90^{rk}
phosphorylation, 1868
protein-serine/threonine kinase, coordinate regulation with, 1868
regulation, 1868
- pp90^{rk} phosphorylation, regulation of
Swiss 3T3 cells
cyclic AMP-mediated signal transduction, 1861
growth factor-mediated signal transduction, 1861
phorbol ester-mediated signal trans-

- duction, 1861
 S6 phosphotransferase activity, 1861
- Preadipocytes
 human
 adipose P2 gene expression, 2303
 C/EBP-binding region, 2303
- Pre-B- and B-cell-specific *mb-1* promoter heterogeneously initiated transcription initiation site sequences, requirement for, 5756
 upstream factor-binding sites, requirement for, 5756
- Pre-B lymphoid cell line transformation
 interleukin-7 hyperexpression, 854
- Pre-B-cell differentiation
 Oct-2
 regulation, 4885
 stage-specific function, possible, 4885
- Pre-B-cell leukemia, prenatal mouse
 E μ -*myc* and E μ -*pim-1* transgenes, 1176
- pre-B-cell transformation
 Abelson murine leukemia virus, 1590
 interleukin-7 retroviruses
 autocrine mechanism, 1590
- Pre-mRNA
 cleavage, efficiency of
 poly(A) site-processing factors, 2432
 recognition
 poly(A) site-processing factors, 2432
 short internal exons
 splice site selection, 6075
- Pre-mRNA editing
P. hybrida mitochondria, 4274
 cis- and trans-splicing, before, 4274
- Preosteoblastic cells
 rat
zif28 early gene expression increase by retinoic acid, 2503
- Pre-tRNA processing
S. cerevisiae, 425
- Primary response gene
 TIS11
 Cys-His repeat, unusual and highly conserved, 1754
 gene family, 1754
- Primate tissues
 natriuretic peptide receptor genes
 differential regional expression, 3454
- Procyclin gene
T. brucei
 transcription unit, similar gene shared with variant surface glycoprotein gene, 1473
 variant surface glycoprotein gene, 1473
- Proenkephalin
 T lymphocytes
 transcription activation by nuclear factor κ B, 1017
- Progesterone
 target gene transcription, enhancement of
 heat shock proteins hsp90, hsp56, and hsp70, receptor free of, 4998
- Progestins
 breast cancer
 cell cycle progression stimulation and inhibition, 5032
 epidermal growth factor receptor, increase in expression of, 5032
c-fos, increase in expression of, 5032
- c-myc*, increase in expression of, 5032
 transforming growth factor α , increase in expression of, 5032
- Programmed cell death
 thymocytes, immature
 mRNAs, 4177
- Prohibitin
 DNA synthesis blocker
 evolutionary conservation, 1372
 fibroblasts, 1372
 HeLa cells, 1372
- Proliferating-cell nuclear antigen gene promoter
D. melanogaster
 zerknüllt protein, repression by, 4909
- Promoter function, suppression of
 cis- and trans-acting mutations
S. cerevisiae SPT16/CDC68 mutations, suppression by, 5710
- Promoter module
 A-activator-binding site, 93
 acute-phase genes, 93
 liver specific, 93
 vitellogenin gene, 93
- Promoter-enhancer approximation
 immunoglobulin DJH, 2096
- Promoterless vectors
 Hox1.3 gene targeted gene disruption, 5578
- Pro-opiomelanocortin gene expression
 pituitary
 regulatory elements, synergistic interactions of, 3492
- Prostate gland
 transgenic mice
 neuroblastoma, 4518
- Proteasome
S. cerevisiae
 subunits, three, cloning and functional analysis, 344
- Protein kinase, 68,000-M_r
 double-stranded RNA, activation by, 5497
 functional expression, 5497
 interferon induction, 5497
 RNA-binding analysis, 5497
- Protein kinase A
 recognition sequence
 p59^{src}, structural link to transformation by, 5867
 p68^{c-rel}, structural link to cytoplasmic retention of, 5867
- Protein kinase C
 human *gadd45* gene induction, 1009
 related gene family
 PKC-L, 126
 specific expression in lung, skin, and heart, 126
- Protein kinase, new class, 2057
- Protein kinases, homologous
 activation
 fibroblasts, mitogenic activation of, 2517
 oocyte maturation, 2517
- Protein phosphatase 2A
 constant expression and activity in synchronized cells, 4282
 control by simian virus 40 small-T antigen, 1988
S. cerevisiae
 bud morphogenesis, effects on, 4876
 cell growth, effects on, 4876
 simian virus 40 large-T antigen, dephosphorylation of, 1996
 simian virus 40 p53 protein, dephosphorylation of, 1996
- Protein synthesis initiation
S. cerevisiae
 GCD2, 3203
- Protein tyrosine phosphatase
 CD45
 CD8⁺ T-cell clones, 4415
 T-cell receptor stimuli, impaired responses to, 4415
- Protein-serine/threonine kinase
 pp90^{src}, coordinate regulation with, 1868
- Protein-tyrosine kinase
trkB
 full-length and two truncated receptors, 143
 neural receptor, 143
- Protein-tyrosine kinases
 p21^{ras} GTPase-activating protein activity, 1804
 phosphorylation, 1804
 protein interactions, 1904
 subcellular distribution, 1804
- Protein-tyrosine kinases, two novel new class of protein kinase, 2057
 phosphotransferase-related catalytic domain, 2057
- Proto-oncogene
c-myc
 activation, 3987
 protein truncation, requirement for, 3987
- Proto-oncogene *fps/fes*
 related gene
D. melanogaster, 226
 life cycle, expression at different times during, 226
- Proto-oncogene *PBX1*
 human
PBX2 and *PBX3*, new homeobox genes with extensive homology, 6149
- Provirus integration
 mouse, transgenic, 886
- Provirus, recombinant
 encephalomyocarditis virus
 ribosome entry site, internal, 5848
- Proximal and remote element pairs
 RNA polymerase II transcription activation, 4561
- Pseudomonas* exotoxin
 chimeric toxin
 foreign protein sequence substitution, 1751
 transforming growth factor α , 1751
- Pseudomonas* exotoxin A
 anti-TFR(Fv)-PE40, 2200
 human transferrin receptor, 2200
 single-chain immunotoxins, 2200
- Pseudouridine modification
 ribonucleoprotein particles assembled in vitro
 U5 RNA, 5998
- Pulsed-field electrophoresis
 megabase-sized DNA, 3348
- PUT3 transcriptional activator
 proline-independent binding
 detection by footprinting in vivo, 564
- S. cerevisiae*
 mutations, constitutive and noninducible, 2609

- Pyrimidine dimers
selective removal from transcribed
strands of active genes
xeroderma pigmentosum complemen-
tation group C cells, 4128
- Quail
myotubes
muscle-specific gene transcription, re-
pression of, 3331
pp60^{src} reactivation, 3331
- rad18 mutator
S. cerevisiae
G · C → T · A transversions, 218
G-A or C-T mismatches, correction to
G · C pairs, 218
- RAD52
S. cerevisiae
repair and recombination, effects on,
2013
- Raf-1
associated kinase activity
G_i and S_i increase through, 2794
epidermal growth factor receptor, asso-
ciation with, 913
epidermal growth factor, stimulation
by, 913
expression
G_i and S_i increase through, 2794
kinase activity
epidermal growth factor, stimulation
by, 913
phosphorylation
G_i and S_i increase through, 2794
T cells, human, CD3 stimulated, 2794
- RAP1
S. cerevisiae
BAS1/BAS2- and GCN4-dependent
transcription of *HIS4* gene, 3642
MATa locus, role in regulation of,
1069
- RAP1 binding sites
S. cerevisiae
ribosomal protein gene transcription
control, 2723
- Rap1A (Krev-1) protein
COOH-terminal domain
isoprenylation, 1523
transformation by H-Ras:Rap1A chi-
meric protein, support of, 1523
- Rapamycin sensitivity
S. cerevisiae
FK506-binding protein, human, 1718
isomerase, peptidyl-prolyl *cis-trans*,
1718
- ras
12-O-Tetradecanoylphorbol-13-acetate
response element activation
lovastatin, selective inhibition by,
2307
cell cycle growth arrest
p53 mutant tumor suppressor alleles,
release by, 1344
cellular
inhibition of activity by dominant in-
hibitory Ras mutants, 4053
effector domain mutant
GTPase-activating protein interac-
tions, 3132
NF-1 interactions, 3132
temperature sensitive, 3132
- mouse
GTPase-activating protein, 2785
phospholipids, mitogenically active,
2785
oncogenic
inhibition of activity by dominant in-
hibitory Ras mutants, 4053
S. cerevisiae
mutationally activated, 3894
RP11, down-regulation by, 3894
transformation of NIH 3T3 cells
c-myc, reversal of phenotype by de-
pletion of, 3699
ras1 mutant phenotype suppression
S. pombe
byr2 protein kinase, 3554
ras effector elements
genetic definition, 6158
Ha-ras
v-mos expression, 803
mouse fibroblasts
αB crystallin accumulation, 803
NIH 3T3 fibroblasts
αB crystallin accumulation, 803
transforming growth factor-β1 promoter
activation, 84
Ras mutants, dominant inhibitory
inhibition of activity of cellular or onco-
genic Ras, 4053
ras oncogene
gap junction proteins
phosphorylation and expression, mod-
ulation of, 5364
Ras p21
target activation
amino acid residues required, 3997
ras p21-like GTP-binding proteins
GDP dissociation stimulator, 2873
smg p21 proteins, 2873
stimulatory GDP/GTP exchange protein,
2873
RAS superfamily, 872
RAS-activating domain
S. cerevisiae *SDC25*, 202
Ras-cyclic AMP pathway
S. cerevisiae
RP11, inhibition by, 3894
Ras^H
Mg²⁺-binding site
GTP, activation by, 4822
mutations, dominant inhibitory, 4822
c-ras^H
transformation
p21, critical amino acids of, 6026
n-ras
mouse
negative regulatory element, 1334
promoter, 1334
upstream regulatory sequences, 1334
transformation of PA-1 human teratocar-
cinoma cells, 3573
v-ras^H
transformation
p21, noncritical amino acids of, 6026
ras-related gene
rhoB immediate-early gene, 3682
Rat
α1-acid glycoprotein gene
interleukin-1 response element, inter-
action with NF-AB, 3001
AMPD1 gene
alternative transcript production, 5356
exon recognition, 5356
nucleocytoplasmic partitioning, 5356
DBP
vitellogenin gene-binding protein, rela-
tion to, 4863
embryo cells, cotransformation of
c-Jun proto-oncoprotein transactivat-
ing function, requirement for,
6286
fetal parietal bone, 250
fibroblasts
rhoB immediate-early gene, 3682
germ cells, testis
transferrinlike (hemiferin) mRNA,
1448
heart development
neural cell adhesion molecule,
27 alternatively spliced forms,
1654
hepatoma cells
25-hydroxycholesterol, complementa-
tion group with resistance to,
2049
AGP/EBP(LAP) interaction with mul-
tiple promoter sites, 4959
alpha-1 acid glycoprotein gene, gluco-
corticoid induction of, 4959
cholesterol-7-alpha-hydroxylase gene,
2049
insulinlike growth factor-binding protein
1 gene
induction, 1393
regenerating liver, induction in, 1393
leukocyte antigen MRC OX-44
cell surface proteins, new family of,
2864
growth regulation, 2864
liver cells
cytochrome P-450IA1 gene, 4314
xenobiotic response element-binding
factor, 4314
xenobiotic response elements 1 and 2,
4314
neu promoter
enhancer, novel, 1875
osteoblast-enriched cultures
activin-A binding, 250
biochemical effects, 250
platelet factor 4 gene
enhancer/silencer domain interaction
with GATA site, 6116
transcriptional regulation, 6116
preosteoblastic cells
zif28 early gene expression increase
by retinoic acid, 2503
Rat myocardial cells
cardiac myosin light-chain-2 gene
28-base-pair element, conserved, 2273
α-adrenergic-inducible expression,
2273
cardiac-specific expression, 2273
rDNA genes
G. lamblia
telomeric location, 3326
Receptor tyrosine kinase, novel
axl transforming gene, 5016
primary human myeloid leukemia cells,
5016
Recombination initiation site
S. cerevisiae *ARG4* locus
poly(dA · dT) tract, 322
Recombination, intrachromosomal
chromatid interactions
direct-repeat analysis, 4839

- mouse cells, 4839
- Repair and recombination
S. cerevisiae RAD52, 2013
- Replication forks
 EBNA-1, role in arresting, 6268
 Epstein-Barr virus
 EBNA-1, role in arresting, 6268
 oriP family of tandem repeats, 6268
- Replication initiation
 human cells
 multiple locations, 1464
 plasmid, autonomously replicating, 1464
- Replication initiation sites
 mammalian genomes
 mapping, 3850
 replication intermediates, stabilization and enrichment of, 3850
- Replication protein A
 DNA synthesis initiation
 DNA polymerase α -primase, 2108
- Replication timing control
 extrachromosomally amplified genes, maintenance in, 4779
- Replicative senescence, premature fibroblasts
 overexpression of diverse gene sequences, 3905
 Werner syndrome, 3905
- Replicon initiation
 inhibition
 human, 3711
 topoisomerase-DNA cleavable complexes, stabilization of, 3711
- Retina, embryonic neural
 v-src expression, effects of, 5275
- Retinoblastoma protein
 E1A, phosphorylation by
 independence of direct physical association, 4253
 human
 family of related polypeptides, 5792
- Retinoic acid
 interleukin-2 promoter down-regulation
 cis-regulatory sequences containing octamer motif, 4771
 response pathways
 apolipoprotein AI gene, 3814
 two different, 3814
 zif28 early gene expression increase, 2503
- Retinoic acid receptors
 antagonism between, 4097
- Retinoic acid response element
 phosphoenolpyruvate carboxykinase gene promoter
 retinoic acid binding, 5164
 thyroid hormone receptor binding, 5164
- Retinoic acid-responsive element
 apolipoprotein AI gene
 retinoic acid response pathways, two different, 3814
- Retroposon
 SCIP transcription factor gene, 4642
- Retrotransposons, site specific
 new family member
T. cruzi spliced leader RNA genes, 6139
- Retroviral insertions
 Evi-1 myeloid transforming gene
 transcription activation, 1820
- Retrovirus
 avian
 DNA synthesis, 1419
 integration in vitro, 1419
 collagen I gene interference, 47
 insertional mutagenesis, induction of
 collagen mutation, mechanism of, 5154
 Mov13 mice, 5154
 Moloney murine leukemia virus
 primer-binding site, 1214
 stem cell-specific silencer, 1214
- Rev response element
 Rev-nucleolar B23 protein complex dissociation, 2567
- Reverse transcriptase
 DNA polymerase, derivation of, 1696
- rhoB
 ras-related gene
 epidermal growth factor induction, 3682
 v-Fps induction, 3682
 platelet-derived growth factor induction, 3682
 rat fibroblasts, 3682
- Ribonucleoprotein particles
 mouse embryonal carcinoma cells
 LINE-1 RNA, 4804
- Ribonucleoprotein particles assembled in vitro
 U5 RNA
 pseudouridine modification, 5998
- Ribosomal protein gene transcription control
S. cerevisiae
 RAP1 binding sites, 2723
- Ribosome
 reinitiation
 GCN4 translational control, 486
S. cerevisiae temperature-sensitive mutants
 60S subunit perturbation, 5681
 L16 protein, defect in, 5681
- Ribosome entry site, internal
 encephalomyocarditis virus
 recombinant provirus, efficient coexpression of two genes from, 5848
- rif
 L-myc fusion
 intrachromosomal rearrangements, 4015
 small-cell lung cancer, 4015
- RNA, 20S, naked, 2905
- RNA14 and -15 gene mutations
S. cerevisiae
 mRNA decay rate, abnormal, 3075
- RNA15 protein
S. cerevisiae
 RNA-binding domain, 3075
- RNA helicase
 p68
 conserved intron, 1326
 nucleolar form, 1326
 related yeast genes, 1326
- RNA helicases
 D-E-A-D family
S. cerevisiae translation initiation factor 4A, conserved residues, 3463
- RNA polymerase I
 mutations, temperature sensitive
 largest subunit, 754
 mutation suppression in a zinc-binding motif by transposed mutant genes, 746
- S. cerevisiae*, 746
 second-largest subunit encoded by suppressor gene, 754
- S. cerevisiae*, 746
- RNA polymerase II
D. melanogaster
 hsp70 gene, pause at 5' end of, 5285
 elongation complexes
 15- or 35-base transcripts, structures when paused after, 1508
 mammalian transcription factors IIF, IIS, and IIX
 elongation, role during, 1195
 mutations in conserved region
 mRNA start site selection, accuracy of, 5781
- S. cerevisiae*
 assembly, mutations affecting, 4669
 mutations in conserved region, 5781
 three largest subunits, mutations in, 4669
- transcription
 HeLa nuclear extract, 4599
 c-myc, premature termination in, 4599
- transcription activation
 proximal and remote element pairs, differential ability to cooperate, 4561
- RNA polymerase III
 transcription factors
 far-downstream sequences, binding by, 1382
 tRNA promoter elements, 1382
- RNA polymerase, transcribing
X. borealis
 transcription factor IIIA, displacement from 5S RNA gene, 3978
- RNA polymerases I and II
 mammalian genes, transcription of
 DNA damage and repair, differential introduction of, 2245
- RNA-binding protein
D. melanogaster suppressor of sable gene, 894
- poly(A)-binding protein
 RNA-binding domains and activities, 3419
- simian virus 40
 downstream element of late polyadenylation signal, interaction with, 5312
- RNase P activity, mitochondrial
C. (Torulopsis) glabrata
 227-nucleotide RNA, 1662
 RNase P RNA, bacterial, 1662
- RNase P RNA, bacterial
C. (Torulopsis) glabrata
 227-nucleotide RNase P RNA, homology to, 1662
- Rous sarcoma virus
 gag gene
 nonsense codons, 2760
 unspliced viral RNA, decreased stability of, 2760
- ROX3 gene
S. cerevisiae
 CYC7 gene expression, essential nuclear protein involved in, 5639
- RDP1 (SIN3/UME4)
S. cerevisiae
 requirement for maximal activation and repression of diverse genes, 6306

RPD3*S. cerevisiae*

second factor required for maximum positive and negative transcriptional states, 6317

RPI1*S. cerevisiae*

Ras function, down-regulation of, 3894
Ras-cyclic AMP pathway inhibitor, 3894

RPR1

nuclear RNase P, 721

S. cerevisiae, 721

rRNA processing, primary

mouse

RNA structural motifs, 458
sequence organization, 458

S3 ribosomal protein

human

overexpression in colorectal cancer, 3842

S6 phosphotransferase activity

Swiss 3T3 cells

cyclic AMP-mediated signal transduction, 1861
growth factor-mediated signal transduction, 1861
phorbol ester-mediated signal transduction, 1861
pp90^{ca}, 1861

S49 cells

kinase-negative mutant

cyclic AMP-dependent protein kinase catalytic subunit maturation defect, 705

Saccharomyces cerevisiae

a-factor

C-terminal cysteine modifications, 3603

a-factor degradation

α -mating-type-specific endopeptidase, 1030

G₁ arrest recovery, 1030

AAR1/TUP1 protein

$\alpha 1$ and $\alpha 2$ repression, 3773

cell type control, 3773

G protein β subunit, similar structure, 3773

AAR2

cell type control, 5693

MAT α 1 cistron pre-mRNA splicing, 5693

ACE2

metallothionein expression activator, 476

SW15 homology, 476

ACT1

complementation by chicken β -actin gene, 213

disruption, 213

adenylate cyclase

GTPase-activating protein IRA1, interactions with, 4591

adenylyl cyclase complex

bifunctional component CAP, 1248
CAP, 1248

ADH2 poly(A) site

3'-end formation efficiency, 2004
upstream point mutations, 2004

ADRI

peroxisomal protein genes, positive

regulation of transcription, 699

ADR1 transcription factor

ADH2 activation, 1566

monomers, two, 1566

palindromic sequence binding, symmetrical, 1566

AGA1 product

α -agglutinin, cell surface attachment of, 4196

Apl1 apurinic endonuclease/3'-di-

esterase

DNA damage, control of, 4537

spontaneous mutation, control of, 4537

ARG4 locus

poly(dA · dT) tract, 322

recombination initiation site, 322

ARGR proteins

ARG5.6 promoter, binding to, 2162

ARGR1 protein

arginine anabolic and catabolic pathways, regulation of, 2169

autonomously replicating sequences

cell division cycle, 5301

chromatin structure, 5301

 β -tubulin codon change

failure to produce significant phenotype, 4726

CAP, 1248**CBP1**

mitochondrial function, induction of, 813

mRNA 3' end formation, 813

CDC7

HMR, repression of transcription at, 1080

CDC20 gene product

β -transducin homolog, 5592

microtubule-dependent cellular processes, requirement for subset of, 5592

CDC25 protein

exchange of guanine nucleotides bound to Ras, 2641

CDC42Sc

GTP-binding protein involved in cell polarity, putative, 3537

mutational analysis, 3537

CDC55

cellular morphogenesis, 5767

mammalian type 2A protein phosphatase B subunit, homology to, 5767

CDC68

carboxyl terminus, highly acidic, 5718

proliferation and transcription, regulation of, 5718

cell adhesion glycoprotein

α -agglutinin, 4196

cell cycle

α -factor internalization and response, 5251

cell cycle stage-dependent transcription

short, *cis*-acting DNA sequence, 329

cell separation

protein synthesis requirements, 3691

centromere

in vivo genomic footprint, 154

centromere CDEIII sequence

mitotic chromosome separation, requirements for, 5212

centromere DNA element I

helix-loop-helix protein CPF1, binding

site for, 3545

centromeres, excess

chromosome loss rates, 2919

citrate synthase (CIT2)

intramitochondrial functions, regulation of expression by, 38

nonmitochondrial, 38

clathrin heavy chain deficient

mutations at numerous loci, 3868

suppression hypothesis, 3868

viability, 3868

CYB2 gene

CYP1(HAP1) activator, 3762

cytochrome *b*₂, 3762

transcriptional regulation, 3762

UAS1-B2, 3762

CYC1 gene

TATA elements, two types, 666

CYC8 protein

glucose repression, 3307

protein complex, 3307

CYP1(HAP1) activator

CYB2 gene transcriptional regulation, 3762

CYT1 gene

cytochrome *c*₁, 4934

HAP1 and HAP2/3/4, regulation by, 4934

cytochrome *b*₂

CYB2 gene transcriptional regulation, 3762

cytochrome *c* heme lyase

mitochondrial import of cytochrome *c*,

role in, 5487

cytokinesis

protein synthesis requirements, 3691

DAL80 gene

GATA factors, homology of product to, 6205

nitrogen catabolic genes, multiple, regulator of, 6205

nitrogen catabolite repression, sensitivity to, 6205

DAL81 gene product

nitrogen catabolic genes, requirement for induced expression of, 1161

DNA strand transfer protein α gene, 2576

DNA strand transfer protein β , 2583

double-strand break repair

tandemly repeated genes, unique pathway in, 1222

DST2 gene, 2583*E. coli* tyrosine tRNA, 2744

endoplasmic reticulum

vesicle budding, membrane glycoprotein required for, 5727

ERG8, 620**FKB1**

FK-506-responsive gene, distinct, 4616

FUS1 gene

pheromone response elements, 2952

transcription, basal and pheromone induced, 2952

gal3 phenotype

galactokinase encoded by *GAL1*, suppression by, 5454

GAL4 phosphorylation

GAL11 (SPT13) transcriptional regulator, 2311

GAL11 (SPT13) transcriptional regulator

GAL4 phosphorylation, 2311

GAS1 protein

- glycophospholipid membrane-anchoring determinants, 27
- GCD2**
GCN4 gene, translational repressor of, 3203
 protein synthesis initiation, 3203
- GCN2** protein kinase
GCN4 gene translational activation, 3027
 ribosome association, 3027
- GCN4**
 amino acid-starved cells, 486
 bZIP domain, highly conserved residues in, 4918
 DNA binding, 4918
 ribosomal reinitiation at upstream open reading frames, suppression of, 486
 translational control, 486
 translational regulators, complex formation by, 3217
- GCN4** gene
 GCN2 protein kinase, translational activation by, 3027
- GLN3**
 nitrogen regulatory gene, positive, 6216
 putative zinc finger DNA-binding domain on protein, 6216
 glutamate dehydrogenase, NAD dependent
 carbon regulation, 4455
 glutamate dehydrogenase, NAD-linked
GDH2 gene complex upstream region role in nitrogen regulation, 6229
 glycolytic mRNAs
 differential regulation, 5330
- GRR1**
 glucose repression, requirement for, 5101
 leucine-rich repeats, protein with, 5101
- GTPase-activating protein IRA1**
 adenylate cyclase, interactions with, 4591
- HAP2**
S. pombe homolog, 611
 small essential core protein domain conservation, 611
- heat shock factor
 regulation, resemblance to *S. pombe*, 281
- heat shock factor gene mutation
 cell cycle, temperature sensitive defect, 2647
 mitochondrial import, temperature sensitive defect, 2647
- heat shock proteins, 1062
- heat shock response
 RNA processing during, 1062
- HML** mating-type locus
 ARS elements, 5346
 silencers, 5346
- HMR**, 1080
- HO**
 SIN1 (SPT2) negative regulator of transcription, 4135
- HXT1** gene product
 hexose transporter, 3804
- K1** killer toxin
 functional domains, mutational analysis, 175
- malate dehydrogenase
 three isozymes, evidence for, 370
- MAT α** locus
 RAPI role in regulation of *MAT α* locus, 1069
- mating pheromones
 Ty1 transposition, inhibition of, 2736
 mating-type switching
 "stuck" mutation, heteroduplex formation and mismatch repair of, 5372
- MDH2** gene
 disruption, 370
 isolation, 370
 nucleotide sequence analysis, 370
- meiosis
 sister chromatid exchange, genetic and physical analyses of, 6328
- meiotic recombination
 specific base-pair mismatch repair, 377
 metallothionein expression activator, 476
- metallothionein gene expression
 heat shock transcription factor, 3676
- metallothionein gene transcription
 heat shock transcription factor, activation by, 1232
- mitochondria
 α -ketoglutarate dehydrogenase complex, 3931
- mitotic chromosome separation, requirements for
 centromere CDEIII sequence, 5212
- MOD5**
 N⁶-isopentenyladenosine modification of tRNA, 2382
 translation initiation sites, 2382
- morphogenesis, two new genes involved in
 mutants, synthetic lethal and multicopy suppressor, 1295
- mouse *Tcp-1* homolog
 microtubule-mediated processes, 2629
- nitrogen catabolic genes
DAL81 gene product, 1161
- nuclear division
 protein synthesis requirements, 3691
- nuclear RNase P, 721
- osmotic stability gene, 4235
- PEP3**
 vacuolar biogenesis, requirement for, 5801
- peroxisomes
 catalase A import, 510
 immunofluorescence analysis, 510
- PET54** gene product
COX1 mitochondrial gene, 2399
COX3 mitochondrial gene, 2399
 functional domains, different, 2399
 mitochondrial gene facilitation, 2399
- PHO4**
PHO8 cis-acting sequence, interaction with, 785
- PHO8**
 cis-acting sequence interaction with *PHO4* protein, 785
- PHO84** gene
 inorganic phosphate transporter, 3229
 phosphomevalonate kinase gene, 620
 polyadenylation sites, different classes of, 3060
- pre-tRNA processing, 425
- proteasome
 subunits, three, cloning and functional analysis, 344
- protein phosphatase 2A
 bud morphogenesis, effects on, 4876
 cell growth, effects on, 4876
- PUT3** transcriptional activator
 mutations, constitutive and noninducible, 2609
- rad18** mutator
 G \cdot C \rightarrow T \cdot A transversions, 218
 G-A or C-T mismatches, correction to G \cdot C pairs, 218
- RAD52**
 repair and recombination, effects on, 2013
- RAPI**
 BAS1/BAS2- and *GCN4*-dependent transcription of *HIS4* gene, 3642
MAT α locus, role in regulation of, 1069
- rapamycin sensitivity
 FK506-binding protein, human, 1718
 isomerase, peptidyl-prolyl *cis-trans*, 1718
- RAS** superfamily, 872
- ribosomal protein gene transcription control
 RAPI binding sites, 2723
- RNA14** gene mutation
 mRNA decay rate, abnormal, 3075
- RNA15** gene mutation
 mRNA decay rate, abnormal, 3075
- RNA15** protein
 RNA-binding domain, 3075
- RNA polymerase I mutations, temperature sensitive
 largest subunit, 754
 mutation suppression in a zinc binding motif by transposed mutant genes, 746
 second-largest subunit encoded by suppressor gene, 754
- RNA polymerase II
 assembly, mutations affecting, 4669
 mRNA start site selection, accuracy of, 5781
 mutations in conserved region, 5781
 three largest subunits, mutations in, 4669
- ROX3** gene
CYC7 gene expression, essential nuclear protein involved in, 5639
- RPD1** (*SIN3/UME4*)
 requirement for maximal activation and repression of diverse genes, 6306
- RPD3**
 second factor required for maximum positive and negative transcriptional states, 6317
- RPI1**
 Ras function, down-regulation of, 3894
 Ras-cyclic AMP pathway inhibitor, 3894
- RPRI**, 721
- S. pombe* HAP2 homolog
 small essential core protein domain conservation, 611
- SDC25**
CDC25-like gene, 202
 dispensable, 202
 RAS-activating domain, 202
- SEC4** protein
 mammalian inhibitory GDP/GTP exchange protein for *smg* p25A, ac-

- tion of, 2909
 Sep1 gene, 2593
SHI
 spacing between TATA and transcription initiation sites, 4121
 SIN1 (SPT2) nonspecific DNA-binding protein related to HMG1, 4135
 HO transcription, negative regulation of, 4135
SIN3/UME4 (RPD1)
 requirement for maximal activation and repression of diverse genes, 6306
SIR1 gene
 mating-defective mutants, extragenic suppressor of, 2253
SIR-dependent functions
 synthetic silencer, mediation by, 5648
SIT4 protein phosphatase
 function in late G₁ for progression into S phase, 2133
SLY gene products
 endoplasmic reticulum-to-Golgi transport, 2980
 GTP-binding Ypt1 protein, suppression of defects in, 2980
SLY genes
 YPT1, suppression of functional loss of, 872
Spk1
 phosphorylation of proteins on serine, threonine, and tyrosine, 987
SPT16/CDC68 mutations
 cis- and trans-acting mutations that affect promoter function, suppression of, 5710
SRK1 gene
 bey1 suppression, 3369
 ins1 suppression, 3369
 protein phosphatase function, 3369
Ste2 plasma membrane protein
 β-lactamase gene fusions, 2620
 topological analysis, 2620
STE12 protein
 DNA-binding domain, properties of, 5910
STP5
 acidic nuclear protein with a carboxy-terminal repeat, 3009
 strand exchange protein Sep1 gene, 2593
SW15
 ACE2 homology, 476
 telomeres, excess
 chromosome loss rates, 2919
 temperature-sensitive mutants
 60S ribosomal subunit perturbation, 5681
 ribosomal protein L16, defect in, 5681
TFIID
 carboxy-terminal domain, 4809
 cell growth, normal, 4809
 transcription factor IID
 TATA box-induced conformational change, 63
 two distinct domains, 63
 transcription factor IIIB
 TFIIIC, second-largest subunit of, 5181
 tRNA gene, two components upstream of, 5181
 transcriptional activation
 whole-cell extract, improved, 4555
 translation initiation factor 4A
 conserved residues, 3463
 RNA helicases, D-E-A-D family, 3463
 translation initiation factor 5A
 cell viability, 3105
 hypusine modification, 3105
TRK1 and TRK2
 K⁺ transporters, structurally related, 4266
TUP1 protein
 glucose repression, 3307
 protein complex, 3307
 tyrosine tRNA, 2744
U4 small nuclear RNA
 spliceosome, dissociation from, 5571
 splicing reaction, nonparticipation in, 5571
 uracil permease
 membrane insertion, 1114
 polytopic plasma membrane protein, 1114
URE2 gene product
 glutathione S-transferases, homology to, 822
 nitrogen source, cellular response to, 822
Vps18p
 α-factor prohormone maturation, 5813
 late Golgi functions, 5813
 vacuolar protein sorting, 5813
 zinc finger protein, putative, 5813
 whole-cell extract, improved transcriptional activation, 4555
YAK1 gene
 protein kinase induced by arrest early in the cell cycle, 4045
Satellite 2 transcripts
 newt
 self-cleavage by using extended hammerhead structures, 6109
Schizosaccharomyces pombe
 ADE6 gene
 mitotic and meiotic recombination, stimulation by strong ADH1 promoter, 289
 ADH1 promoter
 mitotic and meiotic recombination at ADE6 gene, stimulation of, 289
 byr2
 protein kinase, 3554
 ras1 mutant phenotype, partial suppression of, 3554
 Cdc2, inactivation of
 Suc1 binding, mutations affecting, 6177
 chromosome I
 centromere, 2206
 mitotic and meiotic functions, DNA regions required for, 2206
 dis3⁺ gene
 110-kDa essential protein, 5839
 mitotic control, 5839
 DNA topoisomerase II
 functional 125-kDa core polypeptide, 6093
 GTPase-activating protein homolog, 3088
 heat shock factor
 regulation, resemblance to mammalian and *S. cerevisiae*, 281
 S. cerevisiae HAP2 homolog
 small essential core protein domain conservation, 611
 Suc1 binding, mutations affecting
 Cdc2, inactivation of, 6177
SCIP transcription factor gene
 expressed retroposon, features of, 4642
SDC25
 S. cerevisiae
 CDC25-like gene, 202
 dispensable, 202
 RAS-activating domain, 202
SEC4 protein
 S. cerevisiae
 mammalian inhibitory GDP/GTP exchange protein for smg p25A, action of, 2909
Self-cleavage
 satellite 2 transcripts, newt
 extended hammerhead structure, 6109
Sep1 gene
 S. cerevisiae
 strand exchange protein 1, 2593
Serine/threonine kinases
 sequence homology to STY, 568
Serum growth factors
 c-erbB-2/HER2 gene product phosphorylation, 979
Serum response elements, cis-acting promoter
 α-actin gene, skeletal, transcription of, 5090
Serum response factor
 α-actin gene transcription, 5090
 DNA-binding activity
 casein kinase II, mechanism of increase by, 3652
 phosphorylation, extensive modification by
 serum-stimulated fibroblasts, 4545
 phosphorylation sites, mutation of, 3652
Sex-lethal sex determination gene
 D. melanogaster
 late transcripts, 3584
 related polypeptides, multiple, 3584
Sgs-3
 chromatin structure
 D. melanogaster, 523
Sgs-7 and -8 genes
 D. melanogaster
 cis-acting sequences required for expression, 2971
SH2 domain
 p60^{src}
 cellular matrix, detergent insoluble, 1207
 deletions, 1207
SHI
 S. cerevisiae
 spacing between TATA and transcription initiation sites, 4121
Signal recognition particle
 Alu domain of RNA, 3949
 heterodimeric protein subunit, 9- and 14-kilodalton
 binding sites, 3949
 evolutionarily conserved sequence motif, 3949
Signal transducer, species specific
 interferon gamma receptor, human
 extracellular domain, interaction with, 5860
Signal transduction
 cyclic AMP mediated, 1861
 growth factor mediated, 1861
 phorbol ester mediated, 1861
 platelet-derived growth factor, epidermal
 growth factor, and fibroblast growth

- factor
aberrant transduction in BALB/c-3T3
cells resistant to growth inhibition
by interferon- β , 3148
- SIL**
T-cell acute lymphoblastic leukemia, dis-
ruption in
structural characterization, 5462
- Silkmouth**
chorion promoter-binding factors
synergistic interactions, 1954
- Simian virus 40**
adenovirus E1A gene products, 2116
DNA synthesis
initiation in vitro, 2350
large-T antigen
dephosphorylation by protein phos-
phatase 2A, 1996
inhibition of dephosphorylation by
small-t antigen, 1996
p3000-associated transforming func-
tion, biological activity comple-
mentary to, 2116
late polyadenylation signal, downstream
element of
RNA-binding protein, specific interac-
tion with, 5312
p53 protein
dephosphorylation by protein phos-
phatase 2A, 1996
inhibition of dephosphorylation by
small-t antigen, 1996
small-T antigen
protein phosphatase 2A, control of,
1988
- Simian virus 40 T antigen**
growth-inhibitory events, 972
transforming growth factor- β 1, 972
- Simian virus 40 transformation**
initiation and maintenance, block of
excess wild-type p53, 3472
- SIN1 (SPT2) nonspecific DNA-binding
protein**
S. cerevisiae
HMG1, relation to, 4135
HO transcription, negative regulation
of, 4135
- SIN3/UME4 (RPD1)**
S. cerevisiae
requirement for maximal activation
and repression of diverse genes,
6306
- Single-stranded-DNA-binding proteins**
muscle gene elements, interaction with,
1944
- SIR1 gene**
S. cerevisiae
mating-defective mutants, extragenic
suppressor of, 2253
- SIR-dependent functions**
S. cerevisiae
synthetic silencer, mediation by, 5648
- Sister chromatid exchange**
S. cerevisiae meiosis
genetic and physical analyses, 6328
- SIT4 protein phosphatase**
S. cerevisiae
function in late G₁ for progression into
S phase, 2133
- Skeletal actin promoter**
muscle-specific gene expression
factor-binding site shared with myosin
light chain enhancer, 3735
- Skeletal myotubes, chick**
myofibrillar genes
differentiation program, 4473
phorbol esters, selective and revers-
ible inhibition by, 4473
- Skin**
PKC-L, specific expression, 126
- SLY gene products**
S. cerevisiae
endoplasmic reticulum-to-Golgi trans-
port, 2980
GTP-binding Ypt1 protein, suppres-
sion of defects in, 2980
- SLY genes**
RAS superfamily, 872
S. cerevisiae
YPT1, suppression of functional loss
of, 872
- Small nuclear ribonucleoprotein particle
U1**
combinatorial splicing of exon pairs,
5919
two-site binding, 5919
- Small nuclear ribonucleoproteins (RNPs)**
T. brucei
spliced leader RNP, structural organi-
zation and protein components,
5516
- Small nuclear RNA, U4**
S. cerevisiae
spliceosome, dissociation from, 5571
splicing reaction, nonparticipation in,
5571
- Small RNP**
human
7SK ribonucleoprotein, 3432
- Small-cell lung cancer**
L-myc and *rfl* fusion
intrachromosomal rearrangements,
4015
- Small-t antigen**
simian virus 40
protein phosphatase 2A, control of,
1988
- smg p21 proteins**
GDP dissociation stimulator, 2873
small, *ras* p21-like GTP-binding proteins,
2873
stimulatory GDP/GTP exchange protein
for, 2873
- smg p25A**
C-terminal region
GDP/GTP exchange protein, interac-
tions with, 1438
membrane interactions, 1438
- Smooth muscle (enteric type) γ -actin gene**
human, 3296
- Somatic cell hybrids**
pancreas-specific gene sequences
transactivation in, 4423
- Sp1**
collagen α 1(I) promoter, murine
interaction with, 4065
nuclear factor I interaction with, 4065
developmental expression
mouse, 2189
mouse
developmental expression, 2189
promoter, human
synergistic activation of, 1935
- Spinach chloroplast**
petD mRNA
chloroplast proteins, specific in vitro
binding to, 4380
- Spk1**
S. cerevisiae
phosphorylation of proteins on serine,
threonine, and tyrosine, 987
- Spleen focus-forming virus**
long terminal repeat, insertion of
erythropoietin receptor gene, unregu-
lated expression of, 5527
- Splice site choice**
complex transcription unit
polyadenylation signals, multiple inef-
ficient, 5291
- Splice site selection**
pre-mRNAs with short internal exons,
6075
- Spliced leader RNA genes**
T. cruzi
site-specific retrotransposons, new
member of a family of, 6139
- Spliceosome**
S. cerevisiae
U4 small nuclear RNA, dissociation
of, 5571
- Spliceosome assembly**
HeLa cell nuclear extract, heat inacti-
vated
rescue, 3425
- Splicing efficiency**
 μ mRNA, 2324
- Spontaneous mutation, control of**
S. cerevisiae Apn1 apurinic endonucle-
ase/3' diesterase, 4537
- Spontaneous mutations, multiple and dis-
persed**
human cell line, malignant
novel pathway of mutation, 3163
- SPT16/CDC68 mutations**
S. cerevisiae
cis- and *trans*-acting mutations that
affect promoter function, suppres-
sion of, 5710
- src**
chicken embryo fibroblasts
glucose transporter isoforms, differen-
tial regulation of, 4448
suppression of transformation
GTPase-activating protein, 2819
GTPase-activating protein C terminus,
2819
transformed cells
epidermal growth factor receptor,
phosphorylation and activation,
309
- c-src**
cDNAs
5' exons, heterogeneity in, 4165
v-src 3' end, mechanisms for genesis
of, 4165
- Src kinases**
viral and cellular
GTPase-activating protein, interac-
tions with, 5059
molecular features, 5059
- src protein, cellular**
oncogenic activity, regulation of
correct spacing between kinase do-
main and Tyr-527, 5832
- v-src**
3' end, mechanisms for genesis of
c-src cDNAs, 4165
amino-terminal 14 amino acids
v-erbB extracellular and transmem-

- brane domains, functional replacement of, 4760
- diacylglycerol level increase
- type D phospholipase-mediated hydrolysis of phosphatidylcholine, 4903
- embryonic neural retina, expression in
- cell adhesion, alteration of, 5275
- glutamine synthetase, prevention of induction of, 5275
- histogenesis, inhibition of, 5275
- inhibition of transformation
- GTPase-activating protein, 2812
- neurile outgrowth, induction of
- nerve growth factor-induced differentiation, mimicking of critical aspects of, 4739
- Src-transformed cell lines
- eukaryotic translation initiation factor 4E phosphorylation, 2896
- SRK1 gene
- S. cerevisiae*
- bcy1* suppression, 3369
- ins1* suppression, 3369
- protein phosphatase function, 3369
- Ste2 plasma membrane protein
- S. cerevisiae*
- β -lactamase gene fusions, 2620
- topological analysis, 2620
- STE12 protein
- S. cerevisiae*
- DNA-binding domain, properties of, 5910
- Steel factor
- kit
- association with cytoplasmic signaling proteins, induction of, 3043
- autophosphorylation, induction of, 3043
- Steel/W transduction pathway
- kit association with cytoplasmic signaling proteins
- steel factor, induction by, 3043
- kit autophosphorylation
- Steel factor, induction by, 3043
- Stem cells, mouse
- embryonic
- genomic modifications, "in-out" targeting procedure for, 1402
- Stem cell-specific silencer
- Moloney murine leukemia virus primer-binding site, 1214
- retrovirus primer-binding site, 1214
- Steroid hormone receptors
- hybrid response elements, functional interaction with, 3247
- Steroid receptor binding
- transactivation
- in situ distinction, 4350
- Stimulatory GDP/GTP exchange protein
- smg* p21 proteins, 2873
- STP5
- S. cerevisiae*
- acidic nuclear protein with a carboxy-terminal repeat, 3009
- Strand breaks without DNA rearrangement
- V(D)J recombination, 3155
- Strand exchange
- FLP recombinase, induction by, 4497
- Strand exchange protein *Sepl* gene
- S. cerevisiae*, 2593
- Strand scission
- FLP recombinase, induction by, 4497
- Stress proteins, mammalian
- HSP70 and HSP28
- nicotine and either ethanol or heat, coinduction by, 6034
- Strongylocentrotus purpuratus*
- UHF-1
- histone H4 gene transcription factor, 1048
- promoter-binding sites, 1048
- "Stuck" mutation
- S. cerevisiae*
- heteroduplex formation, 5372
- mating-type switching, 5372
- mismatch repair, 5372
- STY
- sequence homology to serine/threonine kinases, 568
- tyrosine-phosphorylating enzyme, 568
- Submaxillary gland
- mouse
- major urinary protein gene enhancer, 4244
- Suc1 binding, mutations affecting
- S. pombe*
- Cdc2*, inactivation of, 6177
- Superoxide dismutase
- bovine
- D. melanogaster*, expression in, 632
- oxidative stress resistance, augmentation, 632
- Suppressor of hairy wing protein
- D. melanogaster*
- hsp70* heat shock gene repression, 1894
- Suppressor of sable gene polypeptide
- D. melanogaster*
- RNA-binding proteins, regions similar to, 894
- Surf-1* and -2 genes
- mouse
- bidirectional promoter, 1281
- SW15
- S. cerevisiae*
- ACE2* homology, 476
- Swiss 3T3 cells
- pp90^{rk} phosphorylation, regulation of, 1861
- S6 phosphotransferase activity, regulation of, 1861
- Synapsis
- FLP recombinase, induction by, 4497
- Synchronized cells
- protein phosphatase 2A, constant expression and activity of, 4282
- Synthetic lethal mutants
- S. cerevisiae*
- morphogenesis, two new genes involved in, 1295
- Synthetic silencer
- S. cerevisiae* *SIR*-dependent functions, mediation of, 5648
- T antigen
- DNA synthesis initiation
- DNA polymerase α -primase, 2108
- T cell
- CD8⁺ clones
- CD45 protein tyrosine phosphatase deficiency, 4415
- receptor stimuli, impaired responses to, 4415
- mouse
- specific CD4 gene enhancer, 5506
- T lymphocytes
- nuclear factor κ B
- proenkephalin transcription activation, 1017
- phosphatidylinositol 3-kinase
- interleukin 2, modification of activity by, 4431
- polyomavirus middle T antigen, modification of activity by, 4431
- tal-1* oncogene
- enhancer-binding activity
- E47/E12 helix-loop-helix proteins, 3037
- Tandemly repeated genes
- double-strand break repair, unique pathway, 1222
- S. cerevisiae*, 1222
- Target activation
- Ras p21
- amino acids required, 3997
- Target gene specificity
- DNA-binding domain, domains outside of
- MRF4, 6103
- myogenin, 6103
- Target gene transcription, enhancement of
- progesterone
- heat shock proteins *hsp90*, *hsp56*, and *hsp70*, receptor free of, 4998
- Targeted gene disruption
- Hox1.3 gene
- promoterless vectors, 5578
- TATA box
- transcription factor IID
- conformational change induction, 63
- TATA elements
- S. cerevisiae* CYC1 gene, 666
- TATA and transcription initiation sites, spacing between
- S. cerevisiae* *SHI*, 4121
- tax gene
- human T-cell lymphotropic virus type I
- transforming growth factor β , overexpression of, 5222
- transgenic mice, 5222
- T-cell acute lymphoblastic leukemia
- SIL*, disruption of
- structural characterization, 5462
- T-cell receptor δ gene enhancer
- cis-regulatory element, 2778
- human
- transcriptional activation site, essential, 5671
- T-lymphocyte GATA-3 factors, 2778
- T-cell receptor gamma genes
- lymphocytes, intestinal intraepithelial
- murine athymic chimeras, 5902
- rearrangement and junctional-site sequence analyses, 5902
- Tcp-1*
- mouse
- microtubule-mediated processes, 2629
- S. cerevisiae* homolog, 2629
- Tec2
- E. crassus*
- developmentally programmed excision, 4751
- transposon-like element, 4751
- Telomerase
- processive, 4572

- Telomere**
 rDNA gene location
G. lamblia, 3326
S. cerevisiae
 chromosome loss rates, 2919
 excess, 2919
- Telomere-binding protein**
P. polycephalum, 2282
- Template-directed primer extension**
Tetrahymena ribozyme, catalysis by, 3390
- Temporal poly(A) site switching**
 adenovirus major late transcription unit, 5977
- Teratocarcinoma cells**
 human
 homeobox gene expression, alteration of, 3573
 N-ras transformation, 3573
- Tetradecanoyl phorbol acetate**
 3T3 cell variant, mitogenically nonresponsive, 1002
- Tetrahymena* ribozyme**
 template-directed primer extension catalysis, 3390
- Tetrahymena thermophila***
 high-mobility-group-like chromosomal proteins
 DNA-binding sequence, highly conserved, 166
 macronuclei, 166
 micronuclei, 166
- TFIID**
S. cerevisiae
 carboxy-terminal domain, 4809
 cell growth, normal, 4809
- TFIIIA gene expression**
 developmental regulation
X. laevis B1 factor, 412
- THP-1 monocytic cells**
 tissue factor mRNA
 lipopolysaccharide, transcriptional and posttranscriptional regulation in response to, 4732
- Thy-1* gene promoter**
 mouse
 functional domains, 2216
- Thy-1* negative lymphoma mutants**
 mannolipids, atypical, 3879
- Thy*⁻ mutator phenotype**
 Chinese hamster cell lines
 deoxyribonucleotide metabolism, cell cycle-dependent variations in, 20
- Thymidine kinase**
 cell cycle regulation
 degradation at mitosis, 2538
 residues near carboxyl terminus, 2538
 herpes simplex virus type 1
 cryptic promoter, 4207
 transgenic mice testes, expression in, 4207
- Thymidine kinase gene**
 human
 cell cycle regulatory unit, 2296
- Thymidine kinase-hygromycin phosphotransferase fusion gene**
 dominant positive and negative selection, 3374
- Thymidylate synthase gene**
 mouse
 5'-flanking region, 1023
 growth-stimulated cells, 1023
- Thymocytes, immature**
 programmed cell death
 mRNAs, 4177
- Thyroid gland maturation**
X. laevis
c-erbAa thyroid hormone receptor gene, 5079
- Thyroid hormone receptor**
 DNA binding, differential
 monomeric, homodimeric, and potentially heteromeric forms, 5005
 novel pathway for action
jun and *fos* oncogene activities, interaction with, 6016
 phosphoenolpyruvate carboxykinase gene promoter
 retinoic acid response element, binding to, 5164
- Thyroid transcription factor TTF-1**
 thyroid-specific enhancer-binding protein (T/EBP)
 structural identity with, 4927
- Thyroid-specific enhancer-binding protein (T/EBP)**
 structural identity with, 4927
- cDNA cloning, 4927**
 functional characterization, 4927
- thyroid transcription factor TTF-1**
 structural identity with, 4927
- TII gene**
 epithelial cell line
 growth arrest specificity, 5338
 transforming growth factor β , regulation by, 5338
- TIS11 gene**
 B-cell hybridoma, 1409
 interleukin-6, activation by, 1409
- TIS11 primary response gene**
 gene family
 Cys-His repeat, unusual and highly conserved, 1754
- Tissue factor mRNA**
 THP-1 monocytic cells
 lipopolysaccharide, transcriptional and posttranscriptional regulation in response to, 4732
- Tissue plasminogen activator promoter**
 GC box-binding activity
 brain, mouse, 3139
- T-lymphocyte GATA-3 factors**
cis-regulatory element
 T-cell receptor δ gene enhancer, 2778
- To autoantigen, 40-kilodalton**
 human mitochondrial RNA processing/7-2 RNA
 in vitro association, 5266
- Topoisomerase II**
 sites of action in vivo
 chromatin structure primary determinant, 4973
 DNA sequence specificity not primary determinant, 4973
- Topoisomerase-DNA cleavable complexes**
 stabilization
 replicon initiation, inhibition of, 3711
- Transactivation**
 steroid receptor binding
 in situ distinction, 4350
- Transactivation domains**
 C/EBP, 1480
- Transcription elongation block**
 minute virus of mice attenuator
 cellular elongation factors, regulation by, 3515
- Transcription factor CREB**
 activity, motifs critical for, 1306
 cyclic AMP response, 1306
 glutamine-rich domain, 1306
- Transcription factor IIB**
S. cerevisiae, 5181
 second largest subunit
 TFIIB, interaction with two components of, 5181
- Transcription factor IID**
S. cerevisiae
 TATA box-induced conformational change, 63
 two distinct domains, 63
- Transcription factor IIIA**
X. borealis
 5S RNA gene, displacement from, 3978
 transcribing RNA polymerase, displacement from 5S RNA gene by, 3978
- Transcription factor IIIB**
S. cerevisiae
 TFIIC, second-largest subunit of, 5181
 tRNA gene, two components upstream of, 5181
- Transcription factor SCIP gene**
 expressed retroposon, features of, 4642
- Transcription factor Sp1**
 promoter, human
 synergistic activation of, 1935
- Transcription factor-binding motifs**
 mouse E β meiotic recombination hot spot, 1813
- Transcription factors**
 multicomponent differentiation regulated
 F9 embryonal carcinoma cells, 1686
- Transcription factors, mammalian**
 RNA polymerase II, role during elongation by, 1195
- Transcription factors, ubiquitous**
 helix-loop-helix muscle regulatory factors, 267
- troponin I gene expression, 267**
- Transcriptional activation**
 ecdysterone regulatory elements, 1846
- S. cerevisiae***
 whole-cell extract, improved, 4555
- Transcriptional activator protein**
 PUT3
 footprinting in vivo, 564
 proline-independent binding, 564
- Transcriptional activator PUT3**
S. cerevisiae
 mutations, constitutive and noninducible, 2609
- Transcriptional repression**
 ecdysterone regulatory elements, 1846
- Transferrin receptor, human**
 immunotoxins, single-chain, 2200
- Transferrinlike (hemiferrin) mRNA**
 germ cells, rat testis, 1448
- Transforming gene**
axl
 primary human myeloid leukemia cells, 5016
 receptor tyrosine kinase, novel, 5016
- Transforming growth factor α**
 chimeric toxin
 foreign protein sequence substitution, 1751
Pseudomonas exotoxin, 1751
 progestins, increase in expression by,

- 5032
 Transforming growth factor β
 epithelial cell line
 T11 gene regulation, 5338
 transgenic mice, overexpression in
 human T-cell lymphotropic virus type
 I *tax* gene, 5222
 Transforming growth factor β 1
 histone H1 kinase activity inhibition
 G₁/S-phase growth arrest, 1185
 osteoblast-enriched cultures from fetal
 rat bone
 glucocorticoid regulation of activity
 and binding, 4490
 p34^{cdc2} phosphorylation, inhibition of
 G₁/S-phase growth arrest, 1185
 Transforming growth factor- β
 early gene responses
 growth-suppressive RB function, cells
 lacking, 4952
 Transforming growth factor- β 1
 extracellular matrix protein expression
 control, 972
 growth inhibitory events, 972
 JunB expression control, 972
 simian virus 40 T antigen, 972
 Transforming growth factor- β 1 promoter
 mouse
 characterization, 84
 Ha-ras oncogene, activation by, 84
 Transforming growth factor- β 3
 mRNA translation
 inhibition by 5' untranslated region,
 4306
 myogenesis, 3795
 secretion, 3795
 transcriptional regulation, 3795
 Transgenic mice
 generic intron, increase of gene expres-
 sion by, 3070
 GTP-binding protein gene, 886
 herpes simplex virus type 1 thymidine
 kinase expression
 cryptic promoter, control by, 4207
 human α -globin gene developmental reg-
 ulation, 3786
 human T-cell lymphotropic virus type I
tax gene, 5222
 transforming growth factor β , overex-
 pression of, 5222
 major histocompatibility complex class I
 genes, human
cis sequences controlling expression,
 3564
 efficient position-independent tissue-
 specific expression, 3564
 mitochondrial uncoupling protein gene
 brown fat, 4147
 DNase I hypersensitivity, 4147
 nerve growth factor
 human T-cell lymphotropic virus type
 I *tax* gene, 4635
trans activation, 4635
 neuroblastoma
 prostate gland, restriction to, 4518
 provirus integration, 886
 Transgenic mouse
 central nervous system
 demyelination, 5479
 Translation initiation
 5' untranslated region, 2656
D. melanogaster
 AUG initiator codon, reduction by
 mutations upstream of, 2149
 sequences surrounding the start site,
 2656
 Translation initiation factor 4A
S. cerevisiae
 conserved residues, 3463
 RNA helicases, D-E-A-D family, 3463
 Translation initiation factor 5A
S. cerevisiae
 cell viability, 3105
 hypusine modification, 3105
 Transposon-like element
E. crassus
 developmentally programmed exci-
 sion, 4751
 Tec2, 4751
trans-spliced gene
C. elegans
 5' untranslated region, 1921
 intron insertion, 1921
 TRK1 and TRK2
S. cerevisiae
 K⁺ transporters, structurally related,
 4266
 trkB
 neural receptor protein-tyrosine kinase
 full-length and two truncated recep-
 tors, 143
 tRNA
 cytoplasmic, 2382
 mitochondrial, 2382
 splicing
 eukaryotes, conserved mechanism in,
 5410
 tRNA gene
S. cerevisiae transcription factor IIIB
 stereospecific location upstream of,
 5181
 tRNA promoter elements
 far-downstream sequences
 RNA polymerase III transcription fac-
 tor binding, 1382
 tRNA splicing
 eukaryotes, conserved mechanism in,
 5410
 Tropomyosin I gene
D. melanogaster
 muscle-specific intron enhancer, regu-
 lation by, 1901
 Tropomyosin expression
D. melanogaster
 muscle function, significant effects on,
 6337
 Troponin I gene
 muscle-specific expression
 helix-loop-helix muscle regulatory fac-
 tors, 267
 transcription factors, ubiquitous, 267
 trp-met oncogene product
Xenopus oocytes
 maturation-producing factor activa-
 tion, 5985
Trypanosoma brucei
 minichromosomes
 DNA nucleotide sequence elements,
 3823
 mitochondrial rRNA
 posttranscriptional 3' polyuridine tail
 formation, 5878
 polycistronic pre-mRNA maturation
 hsp70 locus, 3180
 poly(A) addition, 3180
trans splicing, 3180
 procyclin gene transcription unit, 1473
 small nuclear ribonucleoproteins (RNPs)
 spliced leader RNP, structural organi-
 zation and protein components,
 5516
 variant surface glycoprotein gene pro-
 moter
 posttranscriptional control of gene
 expression, 338
 transient activity assays, 338
 variant surface glycoprotein gene tran-
 scription unit, 1473
 VSG gene
 expression site promoters, 2467
 promoter-associated DNA rearrange-
 ment events, 2467
Trypanosoma cruzi
 spliced leader RNA genes
 site-specific retrotransposons, new
 member of family of, 6139
Trypanosoma equiperdum
 expression site-associated gene
 related gene family, 2180
 minicircles
 guide RNA, 1668
 transcripts, three distinct primary,
 1668
 Tst-1
 POU domain gene family member, 1739
 cell surface adhesion molecule Po pro-
 moter, binding to, 1739
 Po promoter binding, 1739
 Tumor cell growth
 p53 expression, 1
 Tumor formation
 JE gene, suppression by, 3125
 Tumor necrosis factor
 mouse
 type I and type II receptors, 3020
 Tumor necrosis factors α and β
 HL60 cells, 2315
 NF- κ B, cyclic AMP-independent activa-
 tion of, 2315
 Tumor suppressor alleles, mutant
 p53
 ras-induced cell cycle growth arrest,
 release of, 1344
 Tumor suppressor p53
 complexes, wild type and mutant, 12
 RNA binding
 covalent linkage, stable, 1598
 Tumors
 clonal growth
 heparin regulation of autocrine growth
 factors, 108
 heparin regulation of mRNA synthe-
 sis, 108
 hormonal regulation of autocrine
 growth factors, 108
 hormonal regulation of mRNA synthe-
 sis, 108
 TUP1 protein
S. cerevisiae
 CYC8 protein, 3307
 glucose repression, 3307
 protein complex, 3307
 Tyl
S. cerevisiae
 transposition, inhibition of, 2736
 Type II glycoproteins, chimeric
 cell surface transport, 2675
 cytoplasmic and anchor domains, 2675
 endocytosis, 2675

- oligomerization, 2675
- Tyrosine kinase**
c-abl
bcr/abl fusion proteins, activation by, 1553
 brain-specific receptor
 Elk, 2496
 Elk, 2496
 FER
 localization, nuclear and cytoplasmic, 1180
 hepatocyte growth factor receptor
 defective posttranslational processing, activation by, 6084
MET proto-oncogene
 autophosphorylation, activation by, 1793
 defective posttranslational processing, activation by, 6084
- Tyrosine phosphorylation**
 erythropoietin receptor, induction by mitogenesis, correlation with, 4895
 fibroblast growth factor receptor carboxy-terminal peptide
 phospholipase C- γ 1 SH2 domain, binding to, 5068
 fibroblasts, mitogenic activation of, 2517
 oocyte maturation, 2517
- Tyrosine tRNA**
E. coli, 2744
S. cerevisiae, 2744
- Tyrosine-phosphorylated cellular proteins**
 epidermal growth factor stimulation, 945 pp60^{src}
- GTPase-activating protein, induction of association with, 945**
- Tyrosine-phosphorylating enzyme**
 STY
 sequence homology to serine/threonine kinases, 568
- Tyrphostin**
 A431 human epidermoid cells, rapid uptake into, 2697
- U1 small nuclear ribonucleoprotein particle**
 combinatorial splicing of exon pairs, 5919
 two-site binding, 5919
- U1 small nuclear RNA**
 recognition, 1829
- U2 small nuclear ribonucleoprotein particle A' protein, interactions with, 1829**
- U2 small nuclear ribonucleoprotein particle A' protein**
 leucine periodicity, 1578
 assembly
 A' protein leucine periodicity, 1578
 protein-protein interactions, 1578
- U2 small nuclear ribonucleoprotein particle A' protein**
 U1 small nuclear RNA, interactions with, 1829
 U2 small nuclear RNA, interactions with, 1829
- U2 small nuclear RNA**
 recognition, 1829
- U2 small nuclear ribonucleoprotein particle A' protein, interactions with, 1829**
- U3 sequences**
 human immunodeficiency virus type 1 mRNA 3' end formation, 1624
- transcription control region, 1624
- U4 small nuclear RNA**
S. cerevisiae
 spliceosome, dissociation from, 5571
 splicing reaction, nonparticipation in, 5571
- U5 RNA**
 ribonucleoprotein particles assembled in vitro
 pseudouridine modification, 5998
- U6 small nuclear ribonucleoprotein**
cis- and *trans*-splicing systems, protein conserved between, 2026
- U small nuclear ribonucleoprotein particle**
 adenovirus E1A transcript splicing in vitro, interactions during, 1258
- UHF-1**
S. purpuratus
 histone H4 gene transcription factor, 1048
 promoter-binding sites, 1048
- Uracil permease**
S. cerevisiae
 membrane insertion, 1114
 polytopic plasma membrane protein, 1114
- URE2 gene product**
S. cerevisiae
 glutathione S-transferases, homology to, 822
 nitrogen source, cellular response to, 822
- USF**
 DNA binding, 5125
 mammalian activator
X. laevis B1 factor, close relation to, 412
 recombinant 43-kDa versus natural 43/44-kDa, 5125
 transcription activation, 5125
- UV radiation**
 cross-resistance
 cisplatin-resistant human cell line, 2075
- UV response, mammalian**
c-jun activation, 2804
- UV-induced mutations**
 excision repair-deficient human fibroblasts, 1927
 excision repair-proficient human fibroblasts, 1927
 strand bias, cell cycle dependent, 1927
- UV-modified DNA**
 cellular factors for recognition
 cisplatin-resistant human cells, overexpression in, 2075
- Vacuolar biogenesis**
S. cerevisiae
PEP3, 5801
- Vacuolar protein sorting**
S. cerevisiae
 Vps18p, 5813
- Valyl-tRNA synthetase**
 cytosolic
N. crassa cyt-20, 4022
 mitochondrial
N. crassa cyt-20, 4022
- Variant surface glycoprotein gene**
 procyclin gene, 1473
T. brucei
 transcription unit, similar gene shared with procyclin gene, 1473
- Variant surface glycoprotein gene promoter**
T. brucei
 posttranscriptional control of gene expression, 338
 transient activity assays, 338
- vav proto-oncogene**
 amino-terminal helix-loop-helix domain, loss of
 transforming potential activation, 1912
- Vectors, insertion and replacement**
 embryonic stem cells
 integration pattern, 4509
 target frequency, 4509
- Vesicle budding**
 endoplasmic reticulum
S. cerevisiae membrane glycoprotein, requirement for, 5727
- VGF gene**
 nervous system-specific mRNA
 nerve growth factor, induction by, 2335
 PC12 cells, 2335
- Vitellogenin II promoter**
 chicken
 positive and negative control elements, complex set of, 2704
- Vitellogenin II promoter control element**
 vitellogenin gene-binding protein, binding to, 4863
- Vitellogenin gene**
 acute-phase genes, 93
 liver-specific expression, 93
 promoter module
 A-activator-binding site, 93
- Vitellogenin gene-binding protein**
 chicken
 leucine zipper transcription factor, 4863
 rat DBP, relation to, 4863
 vitellogenin II promoter control element, binding to, 4863
- V(D)J recombination**
 replicative mechanism, lack of requirement for, 3972
 strand breaks without DNA rearrangement, 3155
- V-(D)-J recombination signal probes**
 HMG1-related DNA-binding protein, isolation of, 4528
- Vps18p**
S. cerevisiae
 α -factor prohormone maturation, 5813
 late Golgi functions, 5813
 vacuolar protein sorting, 5813
 zinc finger protein, putative, 5813
- VSG gene**
T. brucei
 expression site promoters, 2467
 promoter-associated DNA rearrangement events, 2467
- v-ski**
 transformation defective
 MyoD and myogenin expression induction, 1167
 myotube formation, no induction of, 1167
- Werner syndrome**
 premature replicative senescence
 fibroblasts, 3905

- overexpression of diverse gene sequences, 3905
- wetA*
- A. nidulans*
- spore-specific gene expression, activation of, 55
- spore-specific gene expression, regulation of, 47
- Wilms' tumor gene (WT1)
- mouse
- kidney development, 1707
- WT1
- Wilms' tumor gene, 1707
- Xenobiotic response elements 1 and 2
- rat cytochrome P-450IA1 gene binding factor, 4314
- DNase I-hypersensitive sites, 4314
- Xenopus borealis*
- transcription factor IIIA
- 5S RNA gene, displacement from, 3978
- transcribing RNA polymerase, displacement from 5S RNA gene by, 3978
- Xenopus laevis*
- B1 factor
- mammalian activator USF, close relation to, 412
- TFIIIA gene expression, developmental regulation, 412
- cyclins B1 and B2
- phosphorylation, lack of requirement for cell-cycle transitions, 3860
- early embryonic development
- c-erbA α* thyroid hormone receptor gene, 5079
- fibroblast growth factor receptors
- developmental expression, 2481
- H2B histone gene promoter
- variant octamer motif not required for transcription in oocytes, 641
- kinesin-related protein, 3395
- meiotic induction
- cyclin B, 1713
- mos^{Xe}* coexpression, acceleration by, 1713
- mRNA, developmentally regulated, degradation of
- 3' region, control by, 3115
- maternal mRNA, requirement for translation of, 3115
- oocytes
- chromatin assembly, inhibition of, 5259
- eggs, 1965
- H2B histone gene promoter, 641
- maturation-producing factor activation, 5985
- microtubule-associated protein kinase homolog, cell cycle tyrosine phosphorylation, 1965
- mouse mammary tumor virus promoter derepression, 5259
- p34^{cdc2}*, cell cycle tyrosine phosphorylation, 1965
- trp-met* oncogene product, 5985
- plasmid DNA, microinjected
- differential compartmentalization, 299
- replication efficiency, 299
- Xenopus laevis* oocyte nuclei
- homologous recombination
- single-stranded tails, 3268
- Xenopus laevis* oocytes
- homologous recombination
- nonconservative mechanism, 3278
- recombination intermediates, 3278
- Xeroderma pigmentosum
- complementation group C cells
- pyrimidine dimers, selective removal of, 4128
- YAK1* gene
- S. cerevisiae*
- protein kinase induced by arrest early in the cell cycle, 4045
- Yeast mating-type genes
- major histocompatibility complex genes, mammalian
- regulatory mechanisms, striking similarities, 4228
- YPT1*
- RAS* superfamily, 872
- S. cerevisiae*
- SLY* genes, suppression of functional loss by, 872
- zerknüllt protein
- D. melanogaster*
- proliferating-cell nuclear antigen gene promoter repression, 4909
- zif28* early gene expression
- rat preosteoblastic cells
- retinoic acid, increase by, 2503
- Zinc DNA-binding domain, binuclear
- N. crassa nit-4* protein, 5735
- Zinc finger
- E1A *trans*-activating domain
- transcription factor binding, 4287
- trans*-dominant mutants, 4287
- Zinc finger DNA-binding domain, putative
- S. cerevisiae GLN3* protein, 6216
- Zinc finger protein GLI
- adenovirus E1A
- cooperation with for transformation, 1724
- Zinc finger protein, putative
- S. cerevisiae Vps18p*, 5813
- Zinc finger proto-oncogene *Evi-1*
- DNA-binding protein, sequence specific, 2665
- Zinc finger transcriptional activator
- NGFI-C early response gene, 3835
- Zona pellucida activity
- mouse
- oocyte-specific factors binding to conserved upstream sequence, 6197

